



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181755

TO: Celine Qian
Location: rem/2A64/2C70
Art Unit: 1636
March 16, 2006
Case Serial Number: 09/515363

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 3/8/06
Art Unit: 1636 Phone Number: 2- 0777 Serial Number: 09/515363
Location (Bldg/Room#): 2464 (Mailbox #): 2670 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Melanoma Diff. Assoc. Gene, Promoter & uses thereof.
Inventors (please provide full names): Fish, Paul et al.

Earliest Priority Date: 2/29/2000

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 1

and a nucleic acid encoding SEQ ID NO: 2

Please search above sequences in both commercial database & interference database.

1 NA 3365

✓ 2 AA 1025

Point of Contact
P. Sheppard

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LOCUS CS108225 3380 bp DNA linear PAT 22-JUN-2005
 DEFINITION Sequence 233 from Patent WO2005051988.
 ACCESSION CS108225
 VERSION CS108225.1 GI:68147706
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1
 AUTHORS Abbas, A., Bodary, S., Clark, H., Schoenfeld, J., Williams, P. M.,
 Wood, W. I. and Wu, T. D.
 TITLE Compositions and methods for the treatment of systemic lupus
 erythematosus
 JOURNAL Patent: WO 2005051988-A 233 09-JUN-2005;
 Genentech, Inc. (US)
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 /db_xref="taxon:9606"
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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 4
LOCUS AF095844
DEFINITION Homo sapiens melanoma differentiation associated protein-5 (MDAS)
ACCESSION AF095844
VERSION AF095844.1 GI:11344593
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Homidae; Homo.
TITLE
REFERENCE
AUTHORS Kang, D.C., Gopalakrishnan, R.V., Wu, Q., Jankowsky, E., Pyle, A.M. and Fisher, P.B.
mda-5: An interferon-inducible putative RNA helicase with double-stranded RNA-dependent ATPase activity and melanoma growth-suppressive properties
Proc. Natl. Acad. Sci. U.S.A. 99 (2), 637-642 (2002)
JOURNAL 11805321
PUBMED (bases 1 to 3380)
REFERENCE 2 (bases 1 to 3380)
AUTHORS Kang, D.-C. and Fisher, P.B.
TITLE Direct Submision
JOURNAL Submitted (30-SEP-1998) Urology, Columbia University, P&S, 630 W168th, New York, NY 10032, USA
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REFERENCE
1 Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.
AUTHORS
TITLE Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 2005016962-A 3369 24-FEB-2005;
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RESULT 6
CS036676 3434 bp DNA linear PAT 10-MAR-2005
LOCUS CS036676
DEFINITION Sequence 6182 from Patent WO2005016962.
ACCESSION CS036676
VERSION CS036676.1 GI:60734150
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Abbas A., Clark H., Ouyang W., Williams M.P., Wood W.I. and Wu T.D.
AUTHORS
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 2005016962-A 6182 24-FEB-2005;
Genentech, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 99.9%; Score 3361.8; DB 6; Length 3434;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	55	GGGGCCGGCCTTGAGAGCCCTGTGAGCAACCTCGCAATTGTGACGCAACAGAGCGGTGAC	114
Qy	61	CCTGCTTCTCTAAGTGGGGCAGCGGACAGCGGCAAGCAATTTCACTGTGCCGAGACAA	120
Db	115	CCTGCTTCTCTAAGTGGGGCAGCGGACAGCGGCAAGCAATTTCACTGTGCCGAGACAA	174
Qy	121	CAGACCACTGTGCTTTGGGAGAACCTCTCCCTTCTTGAGAAAGAAAGATGTGCAATGGG	180
Db	175	CAGACCACTGTGCTTTGGGAGAACCTCTCCCTTCTTGAGAAAGAAAGATGTGCAATGGG	234
Qy	181	TATTTCCACAGACGAGAAATTTCCGCTATCTCATCTCTGCTTCAGGGCCAGGGTGAATATG	240
Db	235	TATTTCCACAGACGAGAAATTTCCGCTATCTCATCTCTGCTTCAGGGCCAGGGTGAATATG	294
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Db	295	TACATCCAGGTGGAGCCCTGTGCTGAGACTACCTGACCTTTCTGCTGCGAGAGTGAAGAG	354
Qy	301	CAGATTCAGAGAGCAGTGGCCACCTCCGGGAAATGACAGGAGTTGAACTGTCTGTAGC	360
Db	355	CAGATTCAGAGAGCAGTGGCCACCTCCGGGAAATGACAGGAGTTGAACTGTCTGTAGC	414
Qy	361	ACCTTTGAGAAAGGAGACTGTGGCACTTGTTGTGACTGGGAAATTTGTGTAGAGCCCTCCG	420
Db	415	ACCTTTGAGAAAGGAGACTGTGGCACTTGTTGTGACTGGGAAATTTGTGTAGAGCCCTCCG	474
Qy	421	AGAACCCGGCAGCCCTGTGGCCGGCCGCGCTACATGAAACCTGAGCTCAGGAACTTGCCT	480
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Qy	481	CCAATGTTTGAGAAACGCTCATGATGAATATCTCCAATGCTGAACTGTCTTCAAGCCACT	540
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Db	1015	GGAAATGTCACTGCTTATGATGAAAGTTTGTGACATAACACAAATGGGAGATGATGATCA	1074
Qy	1021	GGCAACATAGGAAAGTATTCAGATGAAGAGATGTGGAGAGAGACATCCCGGAGGCA	1080
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[illegible]

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Qy	2401	GCTGAGTAGAGAGTCAAAAAGCCCAACCATTTGATTGGAGCTGGACACAGCAGTAGATTCAA	2460
Db	2455	GCTGAGTAGAGAGTCAAAAAGCCCAACCATTTGATTGGAGCTGGACACAGCAGTAGATTCAA	2514
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Db	2515	CCCAATGACACGAATGTGAACAAAAAGAACTCATTTGTAAATTTCCGACGTGAAAAATCAAT	2574
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RESULT 7			
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Db 3415 CTCTG 3419
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RESULT 8
CS045628 3434 bp DNA linear PAT 22-MAR-2005
LOCUS CS045628
DEFINITION Sequence 6182 from Patent WO2005019258.
ACCESSION CS045628
VERSION CS045628.1 GI:61851939
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS 1. Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D.
TITLE Diseases and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 2005019258-A 6182 03-MAR-2005;
Genentech, Inc. (US)
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1.3434
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/db_xref="taxon:9606"

ORIGIN

Query Match 99.9%; Score 3361.8; DB 6; Length 3434;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| | | | |
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| | | | |
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LOCUS AX300832
DEFINITION Sequence 1 from Patent WO0185955.
ACCESSION AX300832
VERSION AX300832.1 GI:17382110
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Bahr, G., Cocude, C. and Capron, A.
TITLE Rh16 polypeptides and its fragments and polynucleotides encoding
JOURNAL said polypeptides and therapeutic uses
Patent: WO 0185955-A 1 15-NOV-2001;
Istac (FR) ; INSTITUT PASTEUR DE LILLE (FR)
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ORIGIN
Query Match 99.2%; Score 3338.8; DB 6; Length 3372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3343; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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VERSION AY017378.1 GI:12621065
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REFERENCE 1 (bases 1 to 3373)
AUTHORS Cocude, C., Truong, M.-J., Billaut-Mulot, O., Delasart, V.,
Darcissac, E., Capron, A., Mouton, Y. and Bahr, G.M.
TITLE A novel cellular RNA helicase, RH16, differentially regulates cell
growth, programmed cell death and human immunodeficiency virus type
1 replication
JOURNAL J. Gen. Virol. 84 (12), 3215-3225 (2003)
REFERENCE 2 (bases 1 to 3373)
AUTHORS Cocude, C., Kolesnitchenko, V., Billaut-Mulot, O., Truong, M.-J.,
Capron, A. and Bahr, G.M.
TITLE Identification of a new RNA helicase (RH16) regulated by the
immunomodulator Murabutide
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 3373)
AUTHORS Cocude, C., Kolesnitchenko, V., Billaut-Mulot, O., Truong, M.-J.,
Capron, A. and Bahr, G.M.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2001) Laboratoire d'Immunologie Moléculaire de
l'infection et de l'inflammation, Institut Pasteur de Lille, 1 rue
du Professeur Calmette BP 245, Lille 59019, France
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SOURCE			
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	Hominoidea; Homo.		
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TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2540)		
AUTHORS	Strauberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JUL-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nri.nih.gov Blaker,N., Aylee,K., Beckertom-Stenberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooke,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Latic,P., Legaspi,R., Maduro,Q.L., Masello,C., Maeser,B., Mastrian,S.D., McCloskey,J.C., McQuinn,J., Pearson,R., Stamiripod,S., Thomas,P.J., Touchman,J.W., Tsurgou,C., Vogt,J.L., Walker,M.A., Wechtery,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 174 Row: p Column: 16

FEATURES

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27886567

Location/Qualifiers

gene

CDS

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ORIGIN

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LOCUS CQ777379
DEFINITION Sequence 1065 from Patent EP1394274.
ACCESSION CQ777379

VERSION CQ777379.1 GI:45380363
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuohara,K.
AUTHORS Methode of testing for bronchial asthma or chronic obstructive
TITLE Pulmonary disease
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 Mus musculus
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 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Kang, D.-C. and Fisher, P.B.
 TITLE 1 (bases 1 to 3771)
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 REFERENCE 2 (bases 1 to 3771)
 AUTHORS Kang, D.-C. and Fisher, P.B.
 JOURNAL Direct Submission
 TITLE Submitted (26-Apr-2001) urology, Columbia University, P & S, 630
 West 168th, New York, NY 10032, USA
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REFERENCE	1 (bases 1 to 3635)	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bietow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ushed, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shchepochko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Greenwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalusi, D.E., Schmecher, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)	
REFERENCE	2 (bases 1 to 3635)	
AUTHORS	Director MGC Project.	
TITLE	Direct Submissions	
JOURNAL	Submitted (16-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Ahter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlina, E., Khong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskett, B., Mastrian, S.D., McLoakey, J.C., McDowell, J., Pearson, R., Stancitop, S., Thomas, P.J., Touchman, J.W., Taurignon, C., Vogt, J.T., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Series: IRAX Plate: 177 Row: a Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23956207. location/Qualifiers	
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ORIGIN
Query Match      59.3%; Score 1995.4; DB 9; Length 3635;
Best Local Similarity 77.3%; Pred. No. 0;
Matches 2544; Conservative 0; Mismatches 591; Indels 154; Gaps 4;

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603  AATTGAAGACAAACCGGATTGCTGTGCAAGAAACATATGAATGAATCAGGTGAAG 662
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QY 663  AGAGCTACTAAAGAAAGTTGTGCAGAAAGAAACCTGGTCTGTGATTTCTGATGTTCT 722
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QY 903  AGAATCATTTTTCAGATTTCTGTAGTTTCAGATCAGACACAGTTTGGCAGAAAG 962
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Db      2075 GAAATTTTGAACCTGAGAGAAAGAGATGATTTCTCATGATTTTCTTTGATTAACA 2134
Qy      2220 TAAATGTGAAAAAGCTGCTGAAAAACCAAGATTAAGAAATGAAGCTGACCAAT 2279
Db      2135 GAAATGTGAAAAAGCTGCTGAAAAACCAAGATTAAGAAATGAAGAACTCATTAAT 2194
Qy      2280 AAGAAATACATTAATGAGCAATATATCTGAGACTGAGAAATCGACAGAGAAATTA 2339
Db      2195 AAGAAACAGATCTGAAACATTCACAAAGTCTGAGAGTCTCCCGAGAAATTA 2254
Qy      2340 TACAAAAACAGCAGACAGAGTGCATATGCGCTTCCAGTGAATTAAGAAATGA 2399
Db      2255 TACAAAAACAGCAGACAGACCTTACGACCTTCCAGTGAATTAAGAAATGA 2314
Qy      2400 TCTGAGTAGAGAGTCAAAAGCCACCATCTGATTTGAGCTGACACAGAGTGA 2459
Db      2315 TCGGAGAGTGGAGTCAAAAGCGATCACTGATTTGCGCGGCGACAGAGTGA 2374
Qy      2460 ACCCATGACACAGAAATGAACAAAAGAGTCAATTAATTTGCACTGAGAAATCA 2519
Db      2375 GCCCATGACTCAGACTGAAACAAAAGAGTCAATTAATTTGCACTGCGAAATTA 2434
Qy      2520 TCTGCTTATCGCTACACAGTGGCAGAAAGGTCTGATATTAAGAAATTA 2579
Db      2435 TCTGCTTATCGCTACACAGTGGCAGAAAGGTCTGATATTAAGAAATTA 2494
Qy      2580 TATCGCTTATGCTGCTGACCAATTAAGTCAATGATGATGATGATGATGATGATGAT 2639
Db      2495 TATCGCTTATGCTGCTGACCAATTAAGTCAATGATGATGATGATGATGATGAT 2554
Qy      2640 AACTGATGAGAGACCTTACCTCTGCTGCTCAAGTGTTCAGAGTTATGACATGA 2699
Db      2555 AACTGATGAGAGACCTTATGCTGCTGCTCAAGCAGTGGCTCAGAGTTACGAA 2614
Qy      2700 GACAGTTATGATTTCCGAGAGAAAGTATGATTAAGCTATTAATGATTTGTTCAAAAT 2759
Db      2615 GATTTGTTATGATTTCCGAGAGAAAGTATGATTAAGCTATTAATGATTTGTTCAAAACAT 2674
Qy      2760 GAAACAGAGAGATGATCATTAAGATTTTGAATTAAGATGACAAAGTATTAATGAGAAA 2819
Db      2675 GAAACAGAGAGATGATCATTAAGATTTTGAATTTGAGATTTGAGATTTGAGATTTGAGAT 2734
Qy      2820 GAAATGAAACCAAGAGAAATTAATGCAAGATTTCAAGAAATTAACCATTAATTAAC 2879

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Db      2735 GAAATGAAAGTCAAAAAAGACATTTGCAAAAGCAATTAACAGCAATTCATCGTTAATTAAC 2794
Qy      2880 TTTCTTTTCAAAAACTGACAGTGTGCTAGCTGTTCTGCGGAGAAAGATATCATGTAATTTGA 2939
Db      2795 ACTTCTCTCAAAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2854
Qy      2940 GAAATGATCACTGCAATATGACCCAGAAATTCAGAGAACTTTACATTTGTAAGAGAAA 2999
Db      2855 GAAGATGATCACTGCAATATGACCCAGAAATTCAGAGAACTTTACATTTGTAAGAGAAA 2914
Qy      3000 CAAGACATGCAAAAAAGTGTGCCGACATTAATTAATTTGATGATGATGATGATGATGATGAT 3059
Db      2915 CAAGACATGCAAAAAAGTGTGCCGACATTAATTAATTTGATGATGATGATGATGATGATGAT 2974
Qy      3060 TGGCCAGGCTTGGGAGAACATGATGATGACAAAGGCTTAGATTTGCTTGTCAAAAT 3119
Db      2975 TGGCCAGGCTTGGGAGAACATGATGATGACAAAGGCTTAGATTTGCTTGTCAAAAT 3034
Qy      3120 AAGAAATTTTGTATGATGATTTTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3179
Db      3035 AAGAAATTTTGTATGATGATTTTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3094
Qy      3180 AGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3239
Db      3095 GGAATTTGCTTATGATGATTTTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3154
Qy      3240 GATTAAGACTGATTAAGATTTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3299
Db      3155 AGATTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3214
Qy      3300 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3348
Db      3215 TTAATTTGTTTGTGCTACACTGAGACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3263

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Search completed: March 13, 2006, 23:18:31
 Job time : 16328 secs

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Db      1681 CACATTTTAACTATGTCCTATGATGATTTATTAATTAACCTGTTAAAGAAAC 1740
Qy      1741 CTTGATCAACTGAAAAACCAATATACAGAGCCATGCAAGAAGTTTCCATTCAGATGCA 1800
Db      1741 CTTGATCAACTGAAAAACCAATATACAGAGCCATGCAAGAAGTTTCCATTCAGATGCA 1800
Qy      1801 ACCAGAGAAAGATCCATTTAAAGAGAACTTCTAGAAATATGCAAGATTCAACTTAT 1860
Db      1801 ACCAGAGAAAGATCCATTTAAAGAGAACTTCTAGAAATATGCAAGATTCAACTTAT 1860
Qy      1861 TGTCAATATAGTCCATGTCATGATTTTGGACTGCAACCTATGAGCAATGGGCCATTCA 1920
Db      1861 TGTCAATATAGTCCATGTCATGATTTTGGACTGCAACCTATGAGCAATGGGCCATTCA 1920
Qy      1861 TGTCAATATAGTCCATGTCATGATTTTGGACTGCAACCTATGAGCAATGGGCCATTCA 1920
Db      1921 ATGGAAGAAAAAGCTGCAAAAAAGAGAAATCGCAAGAAAGCTGTTGTGACAGAACTTGG 1980
Qy      1921 ATGGAAGAAAAAGCTGCAAAAAAGAGAAATCGCAAGAAAGCTGTTGTGACAGAACTTGG 1980
Db      1981 AGGAAGTACATGAGGCTCTACAAATTAATGACAAATTCGAATGATAGATGCTATACT 2040
Qy      1981 AGGAAGTACATGAGGCTCTACAAATTAATGACAAATTCGAATGATAGATGCTATACT 2040
Db      1981 AGGAAGTACATGAGGCTCTACAAATTAATGACAAATTCGAATGATAGATGCTATACT 2040
Qy      2041 CATCTTGAATCTTTCTATATATGAGAGAAAGATAGAGATTTGCACTCATTAGAACTGAT 2100
Db      2041 CATCTTGAATCTTTCTATATATGAGAGAAAGATAGAGATTTGCACTCATTAGAACTGAT 2100
Qy      2101 AGTGAATGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Db      2101 AGTGAATGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Qy      2161 AAACCTTTGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Db      2161 AAACCTTTGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Qy      2221 AAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAACTGACCAATTA 2280
Db      2221 AAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAACTGACCAATTA 2280
Qy      2281 AAAAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAACTGACCAATTA 2340
Db      2281 AAAAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAACTGACCAATTA 2340
Qy      2341 AAAAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAACTGACCAATTA 2400
Db      2341 AAAAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAACTGACCAATTA 2400
Qy      2401 GCTGAAGTGAAGTCAAAAGCCCAATCTGATTTGAGCTGCAACAGCAGTGAATCAAA 2460
Db      2401 GCTGAAGTGAAGTCAAAAGCCCAATCTGATTTGAGCTGCAACAGCAGTGAATCAAA 2460
Qy      2461 CCCATGACACAGATGACAAAAAGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db      2461 CCCATGACACAGATGACAAAAAGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Qy      2521 CTGCTTATGCTTACCAAGTGGCAGAAAGATCTGATATTTAAAGATGTAACATTTGTT 2580
Db      2521 CTGCTTATGCTTACCAAGTGGCAGAAAGATCTGATATTTAAAGATGTAACATTTGTT 2580
Qy      2581 ATCCGTTATGCTTCTGTCACCAATGAAATAGCCATGATCCAGGCCCGTGGTCGAGCCAGA 2640
Db      2581 ATCCGTTATGCTTCTGTCACCAATGAAATAGCCATGATCCAGGCCCGTGGTCGAGCCAGA 2640
Qy      2641 GCTGATGAGAGACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Db      2641 GCTGATGAGAGACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Qy      2701 ACAGTTAATGATTTCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2760
Db      2701 ACAGTTAATGATTTCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2760
Qy      2761 AAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820

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Db      2761 AAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
Qy      2821 AAAATGAAAAACCAAGAGAAATATTTGCAAGATTAACAAGATTAACCAATTAATACT 2880
Db      2821 AAAATGAAAAACCAAGAGAAATATTTGCAAGATTAACAAGATTAACCAATTAATACT 2880
Qy      2881 TTCTTTTGGCAAAATCTGCAAGTGTGCTAGCTGTCTGCGGGAAGATATTCATGTAATTGG 2940
Db      2881 TTCTTTTGGCAAAATCTGCAAGTGTGCTAGCTGTCTGCGGGAAGATATTCATGTAATTGG 2940
Qy      2941 AAAATGCAATCAAGTCAATATGACCCCAAGATTTCAAGAACTTACATTTGTAAGAAAAAC 3000
Db      2941 AAAATGCAATCAAGTCAATATGACCCCAAGATTTCAAGAACTTACATTTGTAAGAAAAAC 3000
Qy      3001 AAAGCACTGCAAAAGAGTGTGCGCACTATCAATTAATGTAATGTAATGTAATGTAATGTA 3060
Db      3001 AAAGCACTGCAAAAGAGTGTGCGCACTATCAATTAATGTAATGTAATGTAATGTAATGTA 3060
Qy      3061 GGCCAGGCTTGGGGAACATGATGCTGCAAAAGGCTTATGATTTGCTTGTCTCAAAATA 3120
Db      3061 GGCCAGGCTTGGGGAACATGATGCTGCAAAAGGCTTATGATTTGCTTGTCTCAAAATA 3120
Qy      3121 AGGAATTTGTAGTGTGTTTCAAAAAATTAATGCAAAAGAACATPACAAAAAGTGCGTA 3180
Db      3121 AGGAATTTGTAGTGTGTTTCAAAAAATTAATGCAAAAGAACATPACAAAAAGTGCGTA 3180
Qy      3181 GAATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGATGAT 3240
Db      3181 GAATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGATGAT 3240
Qy      3241 GATTAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
Db      3241 GATTAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
Qy      3301 TGATTAATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
Db      3301 TGATTAATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
Qy      3361 CTCTG 3365
Db      3361 CTCTG 3365

RESULT 2
ADJ74904
ID ADJ74904 standard; DNA; 3380 BP.
XX
AC ADJ74904;
XX
XX
DT 20-MAY-2004 (first entry)
XX
DE Marker gene SEQ ID NO:156.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX gene therapy; marker gene; gene; ds.
XX
OS Homo sapiens.
XX
XX EP1394274-A2.
XX
XX PD 03-MAR-2004.
XX
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
XX
PR 06-AUG-2002; 2002JP-00229312.
XX
XX 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX PA Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K.
XX
XX PI WPI; 2004-193155/19.
XX
XX

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XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.

PS Claim 1; SEQ ID NO 156; 241bp; English.

XX The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (1) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

Query Match 100.0%; Score 3365; DB 12; Length 3380;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCCGCGGCTGAGAGCCCTGTGACAACTCGTATTGTGACGACAGCGGTAGAC 60
DB 1 GGGCCGCGGCTGAGAGCCCTGTGACAACTCGTATTGTGACGACAGCGGTAGAC 60
QY 61 CCTGCTTCTTAAGTGGGAGCGGACAGCGGCAAGCAATTTCACTGTCGCGACAGAA 120
DB 61 CCTGCTTCTTAAGTGGGAGCGGACAGCGGCAAGCAATTTCACTGTCGCGACAGAA 120
QY 121 CAGGACCATCTGCTGGGAGAACCTCTCCCTTCTTGAGAAAGAAAGTGTGAAATGG 180
DB 121 CAGGACCATCTGCTGGGAGAACCTCTCCCTTCTTGAGAAAGAAAGTGTGAAATGG 180
QY 181 TATTTCCAGAGAGAAATTTCCGCTATCTCATCTCGTGTTCAGGCGCAGGTTGAAAATG 240
DB 181 TATTTCCAGAGAGAAATTTCCGCTATCTCATCTCGTGTTCAGGCGCAGGTTGAAAATG 240
QY 241 TACATCCAGAGTGAAGCTGTGTGTAAGTACCTGCTTCTGCTGAGAGGTGAAGAG 300
DB 241 TACATCCAGAGTGAAGCTGTGTGTAAGTACCTGCTTCTGCTGAGAGGTGAAGAG 300
QY 301 CAGATTCAAGAGACAGTCCGCACTTCGCGGAAATATCAGGACAGTTGAATCTGCTGAGAC 360
DB 301 CAGATTCAAGAGACAGTCCGCACTTCGCGGAAATATCAGGACAGTTGAATCTGCTGAGAC 360
QY 361 ACCCTTGAGAGAGAGTCTGGACCTTTGGTGAAGTCCGGAATTCGTGAGGCGCTCCGG 420
DB 361 ACCCTTGAGAGAGAGTCTGGACCTTTGGTGAAGTCCGGAATTCGTGAGGCGCTCCGG 420
QY 421 AGAACCGGAGCGCTCTGGCGCGCTACATGAACCTGAGCTACGAGCTTTGCCCTCT 480

DB 421 AGAACCGGAGCGCTCTGGCGCGCTACATGAACCTGAGCTACGAGCTTTGCCCTCT 480
QY 481 CCATGCTTTGAGAACGCTCATGATGAATATCTCCAACTGTGAACTTCCTCCAGCCACT 540
DB 481 CCATGCTTTGAGAACGCTCATGATGAATATCTCCAACTGTGAACTTCCTCCAGCCACT 540
QY 541 CTGTGTGACAAAGCTTTAGTGAAGAGTCTGGAATAGTGCATGAGAGAGAACTGTG 600
DB 541 CTGTGTGACAAAGCTTTAGTGAAGAGTCTGGAATAGTGCATGAGAGAGAACTGTG 600
QY 601 ACAATTGAAGACAGAAACCGGATTCCTGTCAGAAAAACAATGAAATGAATCAGGTGA 660
DB 601 ACAATTGAAGACAGAAACCGGATTCCTGTCAGAAAAACAATGAAATGAATCAGGTGA 660
QY 661 AGAGAGCTACTAAAAAGATTGTGAGAAAGAAAATGCTGTTCTGCAATTTCTGAATGT 720
DB 661 AGAGAGCTACTAAAAAGATTGTGAGAAAGAAAATGCTGTTCTGCAATTTCTGAATGT 720
QY 721 CTTCGTCAACAGAGAAACAATGAATCTGTCAGAGTTAAACAGCTCTGATTTGCTAGAA 780
DB 721 CTTCGTCAACAGAGAAACAATGAATCTGTCAGAGTTAAACAGCTCTGATTTGCTAGAA 780
QY 781 AGCAATGAGAGATTGAATTTATCAAGTTGATGCTCCAGAGTGAAGAGCAACT 840
DB 781 AGCAATGAGAGATTGAATTTATCAAGTTGATGCTCCAGAGTGAAGAGCAACT 840
QY 841 CTTTCAACACAGTTCAGCCAAATCTGAGAGAGAGAGTCTGGGCGATGAGAAATATCTCA 900
DB 841 CTTTCAACACAGTTCAGCCAAATCTGAGAGAGAGAGTCTGGGCGATGAGAAATATCTCA 900
QY 901 TCAGAAATCATCTTTTGCAAGATTTCTGTAGTTTCAAGATCAGACAAAGTTTGGCAGAA 960
DB 901 TCAGAAATCATCTTTTGCAAGATTTCTGTAGTTTCAAGATCAGACAAAGTTTGGCAGAA 960
QY 961 GGAAGTGCAGTCTTATGATGAAGAGTCTGAGACATAACAGCAATGAGGCGATTTCA 1020
DB 961 GGAAGTGCAGTCTTATGATGAAGAGTCTGAGACATAACAGCAATGAGGCGATTTCA 1020
QY 1021 GGCACCATGAGAAAGTATGATGATGAAGATGAGAGAGAGCAATCCCGGAGCA 1080
DB 1021 GGCACCATGAGAAAGTATGATGATGAAGATGAGAGAGAGCAATCCCGGAGCA 1080
QY 1081 GAATCTCAGCTCAGGCTTTACCAATGGAAGTGGCCAGCCAGCTTTGGAAGGAAAGAT 1140
DB 1081 GAATCTCAGCTCAGGCTTTACCAATGGAAGTGGCCAGCCAGCTTTGGAAGGAAAGAT 1140
QY 1141 ATCATCATCTGCTCCCTACAGGAGTGAAGAAACCAAGTGGCTTTACATGCGCAAG 1200
DB 1141 ATCATCATCTGCTCCCTACAGGAGTGAAGAAACCAAGTGGCTTTACATGCGCAAG 1200
QY 1201 GATCACTTAGACAAAGAAAAAAGCATCTGAGCTGAGAAAAAGTTATAGTTCTTGCAAT 1260
DB 1201 GATCACTTAGACAAAGAAAAAAGCATCTGAGCTGAGAAAAAGTTATAGTTCTTGCAAT 1260
QY 1261 AAGGTACTGTAAGTTGAACAGCTCTTCGCAAGAGATTCCAACTTTTGAAGAAATGG 1320
DB 1261 AAGGTACTGTAAGTTGAACAGCTCTTCGCAAGAGATTCCAACTTTTGAAGAAATGG 1320
QY 1321 TATCGTGTATTTGATTAAGTGTATACCCAACTGAAATATCATTTCCAGAAATTTGTC 1380
DB 1321 TATCGTGTATTTGATTAAGTGTATACCCAACTGAAATATCATTTCCAGAAATTTGTC 1380
QY 1381 AAGCTCTGATATATATATCAGTACAGTCAATCTTTGAAAACTCCCTTTAAACTTG 1440
DB 1381 AAGCTCTGATATATATATCAGTACAGTCAATCTTTGAAAACTCCCTTTAAACTTG 1440
QY 1441 GAAAAATGAGAAAGATGCTGTGTTCAATTTGCACTTTTCCCTATATATCATGATA 1500
DB 1441 GAAAAATGAGAAAGATGCTGTGTTCAATTTGCACTTTTCCCTATATATCATGATA 1500
QY 1501 TGTATCATCACCAACAAAGAGCATGTATATATCATGAGGCAATTAATTTGATGAG 1560

Db 1501 TGTCAATCAACCAAGACAGTGTATTAATACATGATGAGCATTTATTTGATGAG 1560
 Qy 1561 AAGTGAAGAAACATAGACTCAAGAAAGAAACAAACAGATATTCCTCTCTCAGATA 1620
 Db 1561 AAGTGAAGAAACATAGACTCAAGAAAGAAACAAACAGATATTCCTCTCTCAGATA 1620
 Qy 1621 CTGGGACTAAGAGCTTCACTGTGTGTGGAGGGGCCAGAGCCAGAACCTGAGAA 1680
 Db 1621 CTGGGACTAAGAGCTTCACTGTGTGTGGAGGGGCCAGAGCCAGAACCTGAGAA 1680
 Qy 1681 CACATTTTAAACTATGTGCTCAATCTTGATGATTAATTAATTAATTAATTAATTA 1740
 Db 1681 CACATTTTAAACTATGTGCTCAATCTTGATGATTAATTAATTAATTAATTAATTA 1740
 Qy 1741 CTGTGATCACTGAAAGAAACCAATATACAGAGCCATGCAAGAGTTGCCATGATGCA 1800
 Db 1741 CTGTGATCACTGAAAGAAACCAATATACAGAGCCATGCAAGAGTTGCCATGATGCA 1800
 Qy 1801 ACCAGAGAGATCCATTTAAAGAGAACTTCTAGAAATATGACAGAGATCAACTTAT 1860
 Db 1801 ACCAGAGAGATCCATTTAAAGAGAACTTCTAGAAATATGACAGAGATCAACTTAT 1860
 Qy 1861 TGTCAAAAGATGTCATGTCATGATTTGGAATCAACCTTATGAACAAATGGCCATGCA 1920
 Db 1861 TGTCAAAAGATGTCATGTCATGATTTGGAATCAACCTTATGAACAAATGGCCATGCA 1920
 Qy 1921 ATGGAAGAAAGATGTCAGAAAGAAATGCGAAAGAAAGCTGTTGTGTCAGAACTTGG 1980
 Db 1921 ATGGAAGAAAGATGTCAGAAAGAAATGCGAAAGAAAGCTGTTGTGTCAGAACTTGG 1980
 Qy 1981 AGGAAGTACATGAGGCGCTTACAAATTAATGACACATTCGATGATAGATGCTATACT 2040
 Db 1981 AGGAAGTACATGAGGCGCTTACAAATTAATGACACATTCGATGATAGATGCTATACT 2040
 Qy 2041 CATCTTGAAGCTTTCTATATATGAGAGAAAGATTAAGAGTTGGCTCATAGAGATGAT 2100
 Db 2041 CATCTTGAAGCTTTCTATATATGAGAGAAAGATTAAGAGTTGGCTCATAGAGATGAT 2100
 Qy 2101 ACTGATGAGGGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Db 2101 ACTGATGAGGGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Qy 2161 AAACCTTTGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
 Db 2161 AAACCTTTGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
 Qy 2221 AAAATGTTGAAAGGCTGCTGAGAAACCCAGAAATGAAATGAAAGCTGACCAATTA 2280
 Db 2221 AAAATGTTGAAAGGCTGCTGAGAAACCCAGAAATGAAATGAAAGCTGACCAATTA 2280
 Qy 2281 AGAATATCCATATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2340
 Db 2281 AGAATATCCATATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2340
 Qy 2341 ACAAAAACAGACAGAGTGCATATGCTTCCAGTGTGATTAATGAAATGAAATTAAT 2400
 Db 2341 ACAAAAACAGACAGAGTGCATATGCTTCCAGTGTGATTAATGAAATGAAATTAAT 2400
 Qy 2401 GCTGAAGTGAAGAGTCAAGCCCAATCTGATGAGCTGAGACACAGCAGTGAATCAAA 2460
 Db 2401 GCTGAAGTGAAGAGTCAAGCCCAATCTGATGAGCTGAGACACAGCAGTGAATCAAA 2460
 Qy 2461 CCCATGACACAGAAATGAACAAAAGAAATGATTAATTAATTAATTAATTAATTAAT 2520
 Db 2461 CCCATGACACAGAAATGAACAAAAGAAATGATTAATTAATTAATTAATTAATTAAT 2520
 Qy 2521 CTGCTTATGCTACACAGTGCAGAGAGAGTCTGATTAATTAATTAATTAATTAATTA 2580
 Db 2521 CTGCTTATGCTACACAGTGCAGAGAGAGTCTGATTAATTAATTAATTAATTAATTA 2580
 Qy 2581 ATCCGTTATGCTCTGCTACCAATGAATAGCCATGCTCAGGCGCTGCTGAGCCAGCA 2640
 Db 2581 ATCCGTTATGCTCTGCTACCAATGAATAGCCATGCTCAGGCGCTGCTGAGCCAGCA 2640

Qy 2641 GCTGATGAGAGCACTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
 Db 2641 GCTGATGAGAGCACTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
 Qy 2701 ACAGTTAATGATTTCCGAGAGAAAGATGATTAATTAATTAATTAATTAATTAATTA 2760
 Db 2701 ACAGTTAATGATTTCCGAGAGAAAGATGATTAATTAATTAATTAATTAATTAATTA 2760
 Qy 2761 AAACAGAGAGATGCTCATAGATTAATTTGAAATTAACAGATCAAGATTAATTAATTA 2820
 Db 2761 AAACAGAGAGATGCTCATAGATTAATTTGAAATTAACAGATCAAGATTAATTAATTA 2820
 Qy 2821 AAAATGAAGAAACCAAGAGAAATATTTCCAGAGATTAACAGATTAACAGATTAATTA 2880
 Db 2821 AAAATGAAGAAACCAAGAGAAATATTTCCAGAGATTAACAGATTAACAGATTAATTA 2880
 Qy 2881 TTCTCTTGAAGAAACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 Db 2881 TTCTCTTGAAGAAACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 Qy 2941 AAAATGATCAGCTCAATATGACCCCAAGATTAACAGAGATTAACAGATTAATTAATTA 3000
 Db 2941 AAAATGATCAGCTCAATATGACCCCAAGATTAACAGAGATTAACAGATTAATTAATTA 3000
 Qy 3001 AAAGCAGTGCAGAAAGAGTGCAGCTATCAATTAATTAATTAATTAATTAATTAATTA 3060
 Db 3001 AAAGCAGTGCAGAAAGAGTGCAGCTATCAATTAATTAATTAATTAATTAATTAATTA 3060
 Qy 3061 GGCAGAGCTTGGGGAACCAATGATGCTGCAAAAGCTTGAATTTGCTGCTCAAAATA 3120
 Db 3061 GGCAGAGCTTGGGGAACCAATGATGCTGCAAAAGCTTGAATTTGCTGCTCAAAATA 3120
 Qy 3121 AGCAATTTTGAAGGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3180
 Db 3121 AGCAATTTTGAAGGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3180
 Qy 3181 GAATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGAT 3240
 Db 3181 GAATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGAT 3240
 Qy 3241 GATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGATGAT 3300
 Db 3241 GATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGATGAT 3300
 Qy 3301 TGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3360
 Db 3301 TGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3360
 Qy 3361 CTCTG 3365
 Db 3361 CTCTG 3365

RESULT 3
 ADR14404
 ID ADR14404 strand: DNA; 3380 BP.
 ADR14404;
 21-OCT-2004 (first entry)
 Human NF-kappaB pathway-associated gene Segid405.
 NF-kappaB pathway; anti-inflammatory; cytoskeletal; hepatotropic; virucide;
 anti-arthritic; anti-infective; gastroenteric; antiasthmatic;
 anti-arthritic; anti-infective; gastroenteric; antiasthmatic;
 immunosuppressive; vulnary; gene therapy; immune disorder;
 inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KM viral replication; host cell survival; evasion of immune response;
 KM rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KM atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KM autoimmune disorder; hyper immune activity;
 KM aberrant acute phase response; hypercongenital condition; birth defect;
 KM necrotic lesion; wound; organ transplant rejection;
 KM aberrant signal transduction; proliferating disorder; cancer;
 KM HIV propagation; gene; ds; human.
 OS Homo sapiens.
 XX MO2004065577-A2.
 XX PD 05-AUG-2004.
 XX 13-JAN-2004; 2004WO-US000798.
 XX PF 14-JAN-2003; 2003US-0440068P.
 XX PR 12-MAY-2003; 2003US-0469757P.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PI Nadler SG, Neubauer MG, Feder JN, Carman J;
 XX DR WPI. 2004-562168/54.
 XX P-PSDB; ADRI4405.
 PT New isolated polynucleotides and polypeptides associated with NF-kappa
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappa pathway.
 XX
 PS Claim 1; SEQ ID NO 405; 237bp; English.

This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappa pathway. The invention may be useful for the production of compounds with an antiinflammatory, cyclostatic, hepatotropic, virucide, antileukemic, antineoplastic, gastrointestinal-gen, antiallergic, antidiabetic, antihypertensive, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnery activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappa pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-igm syndromes, hyohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase response, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappa pathway of the CC invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.

XX SQ Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

Query Match 100.0%; Score 3365; DB 13; Length 3380;

Best Local Similarity 100.0%; Pred. No. 0; Matches 3365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCCGGCTTGAGAGCCCTGTGACAACTGTGATTTGACGACAGACGGTAGAC 60
 DB 1 GCGCGCCGGCTTGAGAGCCCTGTGACAACTGTGATTTGACGACAGACGGTAGAC 60
 QY 61 CTTGCTTCTTAAGTGGGACGAGACGAGCGGACCGACATTTCACTGTGCGGACAGCAA 120

DB 61 CTTGCTTCTTAAGTGGGACGAGACGAGCGGACCGACATTTCACTGTGCGGACAGCAA 120
 QY 121 CAGACCAATCTGCTTGGAGAAACCTCTCTCTCTGAGAAAAGAAAGATGCAATGCG 180
 DB 121 CAGACCAATCTGCTTGGAGAAACCTCTCTCTCTGAGAAAAGAAAGATGCAATGCG 180
 QY 181 TATTTCACAGACGAAATTTTCCGCTATCTCATCTCTGCTTCAGGGCCAGGGGTGAAAATG 240
 DB 181 TATTTCACAGACGAAATTTTCCGCTATCTCATCTCTGCTTCAGGGCCAGGGGTGAAAATG 240
 QY 241 TACATCCAGGTGAGACCTGTGCTGAGACTACCTGACCTTTCTGCGCAGAGGTGAAGAG 300
 DB 241 TACATCCAGGTGAGACCTGTGCTGAGACTACCTGACCTTTCTGCGCAGAGGTGAAGAG 300
 QY 301 CAGATTGAGAGACAGTCCCACTCCGGGAAATGACAGGAGTTGAACTGCTGCTGAC 360
 DB 301 CAGATTGAGAGACAGTCCCACTCCGGGAAATGACAGGAGTTGAACTGCTGCTGAC 360
 QY 361 ACCTTGGAGAAAGGAGTCTTGCACTTGGTGGACTGCGGAAATTCGTGAGAGCCCTCCGG 420
 DB 361 ACCTTGGAGAAAGGAGTCTTGCACTTGGTGGACTGCGGAAATTCGTGAGAGCCCTCCGG 420
 QY 421 AGAACCGGACGCTCTGCGCGCCGCTACATGAACCTGAGCTCAGCGACTTGCCCTCT 480
 DB 421 AGAACCGGACGCTCTGCGCGCCGCTACATGAACCTGAGCTCAGCGACTTGCCCTCT 480
 QY 481 CCATGCTTTGAGAACGCTCATGATGATATATCTCCAACTGCTGAACTCTCTTCCGCCACT 540
 DB 481 CCATGCTTTGAGAACGCTCATGATGATATATCTCCAACTGCTGAACTCTCTTCCGCCACT 540
 QY 541 CTGCTGACAAAGCTTTAGTGAAGAGCTTTGGAATGATGATGAGAGAGAACTGTG 600
 DB 541 CTGCTGACAAAGCTTTAGTGAAGAGCTTTGGAATGATGATGAGAGAGAACTGTG 600
 QY 601 ACAATTGGAAGACAGAAACCGGATTTGCTGTCAGAAAACAATGAAATGAAATCAGGTGA 660
 DB 601 ACAATTGGAAGACAGAAACCGGATTTGCTGTCAGAAAACAATGAAATGAAATCAGGTGA 660
 QY 661 AGAGAGCTACTAAAAAGGATTTGTGCAAGAAAGAAACCTGTTCTGCAATTTCTGAATGTT 720
 DB 661 AGAGAGCTACTAAAAAGGATTTGTGCAAGAAAGAAACCTGTTCTGCAATTTCTGAATGTT 720
 QY 721 CTTGCTCAAAACAGAAACAAATGAACTTTGTCAGAAAGTTTCAAGGCTCTGATTTGCTCAAA 780
 DB 721 CTTGCTCAAAACAGAAACAAATGAACTTTGTCAGAAAGTTTCAAGGCTCTGATTTGCTCAAA 780
 QY 781 AGCAATGAGAGATGAGAAATTTATCACAAGTTGATGCTCTCAAGTGGAAAGCACTT 840
 DB 781 AGCAATGAGAGATGAGAAATTTATCACAAGTTGATGCTCTCAAGTGGAAAGCACTT 840
 QY 841 CTTTCAACACAGATTCAAGCAAAATCTGGAAGAGAGGTCTGGGCGATGAGAAATTACTCA 900
 DB 841 CTTTCAACACAGATTCAAGCAAAATCTGGAAGAGAGGTCTGGGCGATGAGAAATTACTCA 900
 QY 901 TCAGAAATATCTTTTGCAGATTTCTTCTGTAGTTTCAAGATGAGACAAAGTTTGGCAAA 960
 DB 901 TCAGAAATATCTTTTGCAGATTTCTTCTGTAGTTTCAAGATGAGACAAAGTTTGGCAAA 960
 QY 961 GGAAGTGCAGGTGCTTATGATGAAGATCTTGGACATTAACAGCAATGAGCATGATTTCA 1020
 DB 961 GGAAGTGCAGGTGCTTATGATGAAGATCTTGGACATTAACAGCAATGAGCATGATTTCA 1020
 QY 1021 GGCACCATGGAAGATGATTCAGATGAAAGATGTGGCAGCAAGACATCCCGGAGCCA 1080
 DB 1021 GGCACCATGGAAGATGATTCAGATGAAAGATGTGGCAGCAAGACATCCCGGAGCCA 1080
 QY 1081 GAATCTCAGCTCAGGCTTTACCAATGGAAGTTGCCAGCAGACCTTGAAGGGAAGAT 1140
 DB 1081 GAATCTCAGCTCAGGCTTTACCAATGGAAGTTGCCAGCAGACCTTGAAGGGAAGAT 1140
 QY 1141 ATCATCATCTGCTCCCTCAACAGGAGGTGAAAGAAACCAAGTGGCTTTTACATTCGCAAG 1200
 DB 1141 ATCATCATCTGCTCCCTCAACAGGAGGTGAAAGAAACCAAGTGGCTTTTACATTCGCAAG 1200

Qy	1201	GATCACTTGAACAAGAAAAAAGCACTGAGCCTGGAAAGTATAGTCTTGCAAT	1260
Db	1201	GATCACTTGAACAAGAAAAAAGCACTGAGCCTGGAAAGTATAGTCTTGCAAT	1260
Qy	1261	AAGGTACTGCTAGTTGAAACAGCTCTTCGCAAGAGNTTCCAACATTTTGAAGAAATGG	1320
Db	1261	AAGGTACTGCTAGTTGAAACAGCTCTTCGCAAGAGNTTCCAACATTTTGAAGAAATGG	1320
Qy	1321	TATGCTGTTATTGGATTAAAGTGTGATACCCACCTGAAATATATCATTTTCCGAAGTTGTC	1380
Db	1321	TATGCTGTTATTGGATTAAAGTGTGATACCCACCTGAAATATATCATTTTCCGAAGTTGTC	1380
Qy	1381	AAGTCCTGTGATATTAATATACGATACAGCTCAAACTCTTGAAAACTCCCTCTTAAACTTG	1440
Db	1381	AAGTCCTGTGATATTAATATACGATACAGCTCAAACTCTTGAAAACTCCCTCTTAAACTTG	1440
Qy	1441	GAAATATGAGAAGATGCTGTGTTCATTTGTACAGCTTTTCCCTCATATCATTTGATGAA	1500
Db	1441	GAAATATGAGAAGATGCTGTGTTCATTTGTACAGCTTTTCCCTCATATCATTTGATGAA	1500
Qy	1501	TGTCATCACACCAACAAAGAGAGAGTATATAACATCATAGGCAATTAATTGATGAG	1560
Db	1501	TGTCATCACACCAACAAAGAGAGAGTATATAACATCATAGGCAATTAATTGATGAG	1560
Qy	1561	AAGTTGAAAAACATAGACTCAAGAAAAGAAAAACAACAGATGATTCCTCCCTTCACAGTA	1620
Db	1561	AAGTTGAAAAACATAGACTCAAGAAAAGAAAAACAACAGATGATTCCTCCCTTCACAGTA	1620
Qy	1621	CTGGGACTAAACAGCTTCACTGTGTGTTGAAGGGGCAAGAGCAAGCCAAAGCTGAAAGA	1680
Db	1621	CTGGGACTAAACAGCTTCACTGTGTGTTGAAGGGGCAAGAGCAAGCCAAAGCTGAAAGA	1680
Qy	1681	CACATTTTAAAAACTATGTGCCAATCTTGATGCAATTTACTATTTAAACGTGTTAAAGAAAC	1740
Db	1681	CACATTTTAAAAACTATGTGCCAATCTTGATGCAATTTACTATTTAAACGTGTTAAAGAAAC	1740
Qy	1741	CTTGATCACTGAAAAACCAAAATACAGAGCCATGCAGAGAGTTGCCATTCAGATGCA	1800
Db	1741	CTTGATCACTGAAAAACCAAAATACAGAGCCATGCAGAGAGTTGCCATTCAGATGCA	1800
Qy	1801	ACCGAGAGAGATCCATTTAAAGAGAAACTTTCTAGAAAATAAGACAAAGATTCAAACTAT	1860
Db	1801	ACCGAGAGAGATCCATTTAAAGAGAAACTTTCTAGAAAATAAGACAAAGATTCAAACTAT	1860
Qy	1861	TGTCAAATGATGCCAATGTCAGATTTTGAAGTCAACCTTATGAACAATGGGCCATTCAA	1920
Db	1861	TGTCAAATGATGCCAATGTCAGATTTTGAAGTCAACCTTATGAACAATGGGCCATTCAA	1920
Qy	1921	ATGAAAAAAGAGTCCAAAAAAGAAAGAAATGCAAGAACGTGTTGTGCAAAACATTTG	1980
Db	1921	ATGAAAAAAGAGTCCAAAAAAGAAAGAAATGCAAGAACGTGTTGTGCAAAACATTTG	1980
Qy	1981	AGGAAGTACATGAGGGCCCTTCAAAATTATGACAAATTCGAATGATGAGCGATACT	2040
Db	1981	AGGAAGTACATGAGGGCCCTTCAAAATTATGACAAATTCGAATGATGAGCGATACT	2040
Qy	2041	CATCTGGAACCTTTCTAATAAGAGAGAAAGATAAGAGTTGCAAGTATGGAAGATGAT	2100
Db	2041	CATCTGGAACCTTTCTAATAAGAGAGAAAGATAAGAGTTGCAAGTATGGAAGATGAT	2100
Qy	2101	AGTATGAGGGTGTGATGATGATGATTTGTATGTGATGATGAAGATGAGATTTAAG	2160
Db	2101	AGTATGAGGGTGTGATGATGATGATTTGTATGTGATGATGAAGATGAGATTTAAG	2160
Qy	2161	AAACCTTTGAAACTGATGAAACAGATAGATTTCTCATGACCTTATTTTGAAGAACAT	2220
Db	2161	AAACCTTTGAAACTGATGAAACAGATAGATTTCTCATGACCTTATTTTGAAGAACAT	2220
Qy	2221	AAATATGTTGAAAAAGGCTGGCTGAAAAACCAAGATATGAAAATGAAAAGCTCAACAAATTA	2280
Db	2221	AAATATGTTGAAAAAGGCTGGCTGAAAAACCAAGATATGAAAATGAAAAGCTCAACAAATTA	2280

QY	2281	AGAAATACCAATATGAGACATATATCTAGAGACTGAGAAATCAGACACAGAAATTAATCTTT	2340
Dp	2281	AGAAATACCAATATGAGACATATATCTAGAGACTGAGAAATCAGACACAGAAATTAATCTTT	2340
QY	2341	ACAAAAACAGACAGAGTGCAATATGCGCTTTCCAGTGATTACTGAAAAATGAAAAATTT	2400
Dp	2341	ACAAAAACAGACAGAGTGCAATATGCGCTTTCCAGTGATTACTGAAAAATGAAAAATTT	2400
QY	2401	GCTGAAGTAGAGTCAAAAGCCCACTCTGATTTGAGCTGACACAGCACTGAGTTCAAA	2460
Dp	2401	GCTGAAGTAGAGTCAAAAGCCCACTCTGATTTGAGCTGACACAGCACTGAGTTCAAA	2460
QY	2461	CCCATGACACAGATGAAACAAAAAAGATGATAGTAAATTTGGCACTGAAAAATCAAT	2520
Dp	2461	CCCATGACACAGATGAAACAAAAAAGATGATAGTAAATTTGGCACTGAAAAATCAAT	2520
QY	2521	CTGCTTAATGCTACACAGTGGAGAGAAAGGTCTGATATTTAAAGATGTAACTATTGT	2580
Dp	2521	CTGCTTAATGCTACACAGTGGAGAGAAAGGTCTGATATTTAAAGATGTAACTATTGT	2580
QY	2581	ATCCGTTATGCTCTCGTCCACCAATGAAATATGCCATGTCCAGGCCGCTGGTCCAGCCAGA	2640
Dp	2581	ATCCGTTATGCTCTCGTCCACCAATGAAATATGCCATGTCCAGGCCGCTGGTCCAGCCAGA	2640
QY	2641	GCTGATAGAGACCTAAGCTCTGCTGCTCACAGTGGTTCAAGAGTTATCGAACATGAG	2700
Dp	2641	GCTGATAGAGACCTAAGCTCTGCTGCTCACAGTGGTTCAAGAGTTATCGAACATGAG	2700
QY	2701	ACAGTTAATATATTTCCAGAGAAAGATGATGTATTAAGCTATTAATGTGTCTCAAAATATG	2760
Dp	2701	ACAGTTAATATATTTCCAGAGAAAGATGATGTATTAAGCTATTAATGTGTCTCAAAATATG	2760
QY	2761	AAACCAAGAGAGTATGCTCATTAAGATTTGAAATTAAGATGCAAAAGTATATGAAAAG	2820
Dp	2761	AAACCAAGAGAGTATGCTCATTAAGATTTGAAATTAAGATGCAAAAGTATATGAAAAG	2820
QY	2821	AAAATGAAAAACCAAGAAATATTTGCCAAGACATTAACAAGATTAACCATCACTAATAACT	2880
Dp	2821	AAAATGAAAAACCAAGAAATATTTGCCAAGACATTAACAAGATTAACCATCACTAATAACT	2880
QY	2881	TTCCCTTGCAAAAACTGACGTGTCGCTGTTCTGGGAGAAATATCAATGTAATTGAG	2940
Dp	2881	TTCCCTTGCAAAAACTGACGTGTCGCTGTTCTGGGAGAAATATCAATGTAATTGAG	2940
QY	2941	AAAATGCAACGTCATATAGACCCCAAGATTCAGAGAACTTTACATTTGTAGAGAAAAC	3000
Dp	2941	AAAATGCAACGTCATATAGACCCCAAGATTCAGAGAACTTTACATTTGTAGAGAAAAC	3000
QY	3001	AAAGCACTGCAAAAGAAAGTGTGCCGACTATCAATTAATGTGAAATCATCTGCAATGT	3060
Dp	3001	AAAGCACTGCAAAAGAAAGTGTGCCGACTATCAATTAATGTGAAATCATCTGCAATGT	3060
QY	3061	GGCAGGCTTGGGGAAACAATGATGTCGCAAAAAGGCTTAATTTGCTTGTCTCAAAATA	3120
Dp	3061	GGCAGGCTTGGGGAAACAATGATGTCGCAAAAAGGCTTAATTTGCTTGTCTCAAAATA	3120
QY	3121	AGGAATTTTGTAGTGTCTTCAAAAAATTAATTCACAAAGAAACAATACAAAAAGTGCTTA	3180
Dp	3121	AGGAATTTTGTAGTGTCTTCAAAAAATTAATTCACAAAGAAACAATACAAAAAGTGCTTA	3180
QY	3181	GAATTAACCTATCACTATTTCCCAATCTTGACTATTCAGAAATGCTGTTATTTAGTATGAG	3240
Dp	3181	GAATTAACCTATCACTATTTCCCAATCTTGACTATTCAGAAATGCTGTTATTTAGTATGAG	3240
QY	3241	GATTAGACCTGATGTAAGATCTTTTAAAAATCTATCAAGTAAACATTTAATATGATTA	3300
Dp	3241	GATTAGACCTGATGTAAGATCTTTTAAAAATCTATCAAGTAAACATTTAATATGATTA	3300
QY	3301	TGATTAATGATTCATTAATCTCTACAGAACTGACATTAAGATCAATAAATGATTTGTTTAA	3360
Dp	3301	TGATTAATGATTCATTAATCTCTACAGAACTGACATTAAGATCAATAAATGATTTGTTTAA	3360
QY	3361	CTCTG 3365	

Db 3361 CTCTG 3365

RESULT 4
AEA23691
ID AEA23691 standard; DNA; 3380 BP.

XX AEA23691;

DT 11-AUG-2005 (first entry)

XX Human PRO polypeptide DNA SEQ ID NO 233.

DE Immune disorder; PRO; Antiinflammatory; Dermatological;

XX Immunopressiveive; Antirheumatic; Antiarthritic; Osteopathic;

KW Muscular-gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant;

XX ds; gene.

OS Homo sapiens.

PN WO200501988-A2.

XX 09-JUN-2005.

PF 02-MAR-2004; 2004WO-US006460.

XX 03-MAR-2003; 2003US-0451884P.

PA (GETH) GENENTECH INC.

PI Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WT;

XX Wu TD;

DR MPI: 2005-417958/42.

XX P-P8DB; AEA23692.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and

PT treating an immune related disorder, e.g. systemic lupus erythematosus,

PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or

PT psoriasis.

XX Disclousure; SEQ ID NO 233; 966pp; English.

XX The invention relates to an isolated nucleic acid. The polypeptide,

CC compound or composition, and methods are useful for diagnosing and

CC treating an immune related disorder, e.g. systemic lupus erythematosus,

CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,

CC spondyloarthritis, osteoarthritis, systemic sclerosis, idiopathic inflammatory

CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,

CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases

CC including bullous skin diseases, erythema multiforme and contact

CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The

CC present sequence represents a human PRO polypeptide DNA.

XX Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 3365; DB 14; Length 3380;

XX Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 TATTCACAGACGAAATTTCCGCTATCTCTGCTCTCAGGGCCAGGGGTGAATG 240

Db 181 TATTCACAGACGAAATTTCCGCTATCTCTGCTCTCAGGGCCAGGGGTGAATG 240

QY 241 TACATCCAGGTGAGACCTGTCTGCTGAACTGACCTTCTGCTGACAGAGTGAAGAG 300

Db 241 TACATCCAGGTGAGACCTGTCTGCTGAACTGACCTTCTGCTGACAGAGTGAAGAG 300

QY 301 CAGATTCAGAGACAGTGGCCACCTCCGGAAATGACAGGAGTTGAACTGCTGAGC 360

Db 301 CAGATTCAGAGACAGTGGCCACCTCCGGAAATGACAGGAGTTGAACTGCTGAGC 360

QY 361 ACCTTGAGAAAGGAGTGTGCACTTGTGTGACCTGCGGAATTCGTGGAAGCCCTCCG 420

Db 361 ACCTTGAGAAAGGAGTGTGCACTTGTGTGACCTGCGGAATTCGTGGAAGCCCTCCG 420

QY 421 AGAACCCGACGCTCTGCGCCGCTGACATGAACTGAGCTCAAGGACTTGGCTCT 480

Db 421 AGAACCCGACGCTCTGCGCCGCTGACATGAACTGAGCTCAAGGACTTGGCTCT 480

QY 481 CCATGCTTTGAGAACGCTCATGATGAAATATCTCAACTGCTGAACCTTCAAGCCACT 540

Db 481 CCATGCTTTGAGAACGCTCATGATGAAATATCTCAACTGCTGAACCTTCAAGCCACT 540

QY 541 CTGTGAGCAAGCTTCTAGTGAAGACCTCTTGAATAGTGCATGAGAGAGAACTTTG 600

Db 541 CTGTGAGCAAGCTTCTAGTGAAGACCTCTTGAATAGTGCATGAGAGAGAACTTTG 600

QY 601 ACAATTGAAGACAGAAACCGATTGCTCTGACAGAAACAATGAAATGAAATGAGTGA 660

Db 601 ACAATTGAAGACAGAAACCGATTGCTCTGACAGAAACAATGAAATGAAATGAGTGA 660

QY 661 AGAGAGCTACTAATAAAGATTGTGCAAGAAAGAACTGCTTCTGCAATTTCTGAATGT 720

Db 661 AGAGAGCTACTAATAAAGATTGTGCAAGAAAGAACTGCTTCTGCAATTTCTGAATGT 720

QY 721 CTTCGCTAAACAGAAACAATGAACCTTCCAAAGTTAAAGAGCTCGATTTCTCAAG 780

Db 721 CTTCGCTAAACAGAAACAATGAACCTTCCAAAGTTAAAGAGCTCGATTTCTCAAG 780

QY 781 AGCAATGAGAGATTGAAATTTATCAAGATGATGATGATGATGATGATGATGATGAT 840

Db 781 AGCAATGAGAGATTGAAATTTATCAAGATGATGATGATGATGATGATGATGATGAT 840

QY 841 CTTTCAACACAGATTCAGCCAAATCTGAGAGAGAGGTCTGAGGATGAGAAATTAATCTCA 900

Db 841 CTTTCAACACAGATTCAGCCAAATCTGAGAGAGAGGTCTGAGGATGAGAAATTAATCTCA 900

QY 901 TCAGATATATCTTTTGGCAGATTTCTTGTAGTTTCAAGATCAAGACAAATTTTGGCAGAA 960

Db 901 TCAGATATATCTTTTGGCAGATTTCTTGTAGTTTCAAGATCAAGACAAATTTTGGCAGAA 960

QY 961 GGAAGTGCAGCTGCTTATGATGAAAGCTTGGACATACAGACATAGGCGATGATTTCA 1020

Db 961 GGAAGTGCAGCTGCTTATGATGAAAGCTTGGACATACAGACATAGGCGATGATTTCA 1020

QY 1021 GGCACCATGAGAAAGTATTCAGATGAAAGATGAGAGATGAGAGATTCCTCCGAGCCA 1080

Db 1021 GGCACCATGAGAAAGTATTCAGATGAAAGATGAGAGATGAGAGATTCCTCCGAGCCA 1080

QY 1081 GAACTCCAGCTCAGGCTTTTCAAAATGAAATGAGATGAGATGAGATGAGATGAGAT 1140

Db 1081 GAACTCCAGCTCAGGCTTTTCAAAATGAAATGAGATGAGATGAGATGAGATGAGAT 1140

QY 1141 ATCATCATCTGCTCTTACAGAGAGTGAAGAAACAGAGTGGCTGTTTACATTTCCAG 1200

Db 1141 ATCATCATCTGCTCTTACAGAGAGTGAAGAAACAGAGTGGCTGTTTACATTTCCAG 1200

QY 1201 GATCACTTGAACAGAAAGAAAGATCTGAGCTTGAAGAAAGTTATGTTTGTCAAT 1260

Db 1201 GATCACTTGAACAGAAAGAAAGATCTGAGCTTGAAGAAAGTTATGTTTGTCAAT 1260

QY 1261 AAGGTACTGTAATTTGAACAGCTCTTCCGCAAGAGTTCAACCAATTTTGAAGAAATGG 1320

Db 1261 AAGGATCTGCTAGTGGACAGCTCTCCCAAGAGACTCCAAACCATTTTGGAGAAATG 1320
Qy 1321 TATCGCTATTAGATTAAGTGGTATACCACTGAAAATATCATTCOCAGAGTTGTC 1380
Db 1321 TATCGCTATTAGATTAAGTGGTATACCACTGAAAATATCATTCOCAGAGTTGTC 1380
Qy 1381 AAGTCTGTGATATTAATATATGATACAGTCAATCTTGAAAACCTCCCTTAACTTG 1440
Db 1381 AAGTCTGTGATATTAATATATGATACAGTCAATCTTGAAAACCTCCCTTAACTTG 1440
Qy 1441 GAAATATGAGAAAGATGCTGTGTTCAATTGTGACACTTTTCCCTCATTAATCATGATGA 1500
Db 1441 GAAATATGAGAAAGATGCTGTGTTCAATTGTGACACTTTTCCCTCATTAATCATGATGA 1500
Qy 1501 TGTCAATCACCAACAAAGAGAGTGTATTAATATATGATGAGATTAATTGAGCAG 1560
Db 1501 TGTCAATCACCAACAAAGAGAGTGTATTAATATATGATGAGATTAATTGAGCAG 1560
Qy 1561 AAGTGAAGAAACATATAGACTCAAGAAAGAAAACAAACAGTGTATCCCTTCCCTCAGATA 1620
Db 1561 AAGTGAAGAAACATATAGACTCAAGAAAGAAAACAAACAGTGTATCCCTTCCCTCAGATA 1620
Qy 1621 CTGGGACTTACAGCTTCACTGTGTGTTGAGAGGGGCCACAGAGACCCAAAGCTGAAGAA 1680
Db 1621 CTGGGACTTACAGCTTCACTGTGTGTTGAGAGGGGCCACAGAGACCCAAAGCTGAAGAA 1680
Qy 1681 CACATTTTAAACTATGAGCCAACTTTGATGCACTTATTAATTAACCTTTAAAGAAAC 1740
Db 1681 CACATTTTAAACTATGAGCCAACTTTGATGCACTTATTAATTAACCTTTAAAGAAAC 1740
Qy 1741 CTGTGATCACTGAAACCAAAATATACAGAGCCATGCAAGAGTTGCCATTTGAGAGATGA 1800
Db 1741 CTGTGATCACTGAAACCAAAATATACAGAGCCATGCAAGAGTTGCCATTTGAGAGATGA 1800
Qy 1801 ACCAGAGAGATTCATTAAAGAGAACTTTAGAAATATATGACAGATTCAACTTAT 1860
Db 1801 ACCAGAGAGATTCATTAAAGAGAACTTTAGAAATATATGACAGATTCAACTTAT 1860
Qy 1861 TGTCAATGAGTCCAACTGTCAGATTTTGGAACTCAACCTTATGAAACAAATGGGCAATTC 1920
Db 1861 TGTCAATGAGTCCAACTGTCAGATTTTGGAACTCAACCTTATGAAACAAATGGGCAATTC 1920
Qy 1921 ATGGAAGAAAGAGTGCAGAAAGAAATGCGAAAGAAAGTGTGTGTCAGAACTTGG 1980
Db 1921 ATGGAAGAAAGAGTGCAGAAAGAAATGCGAAAGAAAGTGTGTGTCAGAACTTGG 1980
Qy 1981 AGGAAGTACATGAGGCCCTTACAAATTAATGACAACTTCGATGATAGATGCTATCT 2040
Db 1981 AGGAAGTACATGAGGCCCTTACAAATTAATGACAACTTCGATGATAGATGCTATCT 2040
Qy 2041 CATCTTGAACCTTTCTATATATGAGAGAAAGATAGAGTTGTCAGTCTATAGAAATGAT 2100
Db 2041 CATCTTGAACCTTTCTATATATGAGAGAAAGATAGAGTTGTCAGTCTATAGAAATGAT 2100
Qy 2101 AGTGAATGAGGGTGTATGATAGTATGATGATGATGATGATGATGATGATGATGATG 2160
Db 2101 AGTGAATGAGGGTGTATGATAGTATGATGATGATGATGATGATGATGATGATGATG 2160
Qy 2161 AAACCTTTGAACTGTGATGAAACAGATAGATTTCTCATGACCTTATTTTGGAAAACAT 2220
Db 2161 AAACCTTTGAACTGTGATGAAACAGATAGATTTCTCATGACCTTATTTTGGAAAACAT 2220
Qy 2221 AAAATGTTGAAAGGCTGTGCTGAAAAACCAAGATATGAAAAAGCTGACCAATTA 2280
Db 2221 AAAATGTTGAAAGGCTGTGCTGAAAAACCAAGATATGAAAAAGCTGACCAATTA 2280
Qy 2281 AGAAATACCATATGAGAGCAATATATAGAGCTGAGAGATCAGCAGAGGAATATCTTT 2340
Db 2281 AGAAATACCATATGAGAGCAATATATAGAGCTGAGAGATCAGCAGAGGAATATCTTT 2340
Qy 2341 ACAAAAACGACAGAGTGCATATGCGCTTCCAGTGTATTAATGAAAAATTTT 2400
Db 2341 ACAAAAACGACAGAGTGCATATGCGCTTCCAGTGTATTAATGAAAAATTTT 2400

Db 2341 ACAAAAACGACAGAGTGCATATGCGCTTCCAGTGTATTAATGAAAAATTTT 2400
Qy 2401 GCTGAAGTGAAGTCAAAAGCCCACTGATTTGAGCTGGAACACAGCAGTAGTTCAA 2460
Db 2401 GCTGAAGTGAAGTCAAAAGCCCACTGATTTGAGCTGGAACACAGCAGTAGTTCAA 2460
Qy 2461 CCCATGACACAGATGAAACAAAAGAGTCAATTAATTAATTTGCACTGAAAAATCAT 2520
Db 2461 CCCATGACACAGATGAAACAAAAGAGTCAATTAATTAATTTGCACTGAAAAATCAT 2520
Qy 2521 CTGCTTATGCTACCAAGTGGCAGAGAAAGTCTGATATTTAAAGATGTAATCTTT 2580
Db 2521 CTGCTTATGCTACCAAGTGGCAGAGAAAGTCTGATATTTAAAGATGTAATCTTT 2580
Qy 2581 ATCCGTTATGCTGTGCTGCAACATGAAATATGATGATGATGATGATGATGATGATG 2640
Db 2581 ATCCGTTATGCTGTGCTGCAACATGAAATATGATGATGATGATGATGATGATGATG 2640
Qy 2641 GCTGATGAGAGCACTGACGTCCTGTGCTCAAGTGTTCAGAGTTATTCGAACATGAG 2700
Db 2641 GCTGATGAGAGCACTGACGTCCTGTGCTCAAGTGTTCAGAGTTATTCGAACATGAG 2700
Qy 2701 ACAGTTAATGATTTCCGAGAGAAAGATGATGATGATGATGATGATGATGATGATG 2760
Db 2701 ACAGTTAATGATTTCCGAGAGAAAGATGATGATGATGATGATGATGATGATGATG 2760
Qy 2761 AAACAGAGAGATGCTCATAGATTTTGAATTAACAGATCAAAAGTAAATGAAAG 2820
Db 2761 AAACAGAGAGATGCTCATAGATTTTGAATTTACAGATTCAAAGTAAATGAAAG 2820
Qy 2821 AAAATGAAACCAAGAGAAATATGCGAAGATTAACAAATTAACCATCACTAATTA 2880
Db 2821 AAAATGAAACCAAGAGAAATATGCGAAGATTAACAAATTAACCATCACTAATTA 2880
Qy 2881 TTCTTTGCAAAAACGTCAGTGTGCTAGCTGTCTGCGGAGATATTCATGATTAATGAG 2940
Db 2881 TTCTTTGCAAAAACGTCAGTGTGCTAGCTGTCTGCGGAGATATTCATGATTAATGAG 2940
Qy 2941 AAATGATCATACGTCAATATGACCCAGAAATTCAGAGAACTTATCATGTAAGAGAAAC 3000
Db 2941 AAATGATCATACGTCAATATGACCCAGAAATTCAGAGAACTTATCATGTAAGAGAAAC 3000
Qy 3001 AAAGCATGCAAAAGAGTGTGCGCATATCAAAATTAATGATGAAATCATCTGCAAAATG 3060
Db 3001 AAAGCATGCAAAAGAGTGTGCGCATATCAAAATTAATGATGAAATCATCTGCAAAATG 3060
Qy 3061 GGCAGAGCTTGGGGAACAAATGATGATGATGATGATGATGATGATGATGATGATG 3120
Db 3061 GGCAGAGCTTGGGGAACAAATGATGATGATGATGATGATGATGATGATGATGATG 3120
Qy 3121 AGGAATTTGTATGCTTTTCAAAAATTAATCAAGAAAGAAACAAATTAACAAAGTGGGTA 3180
Db 3121 AGGAATTTGTATGCTTTTCAAAAATTAATCAAGAAAGAAACAAATTAACAAAGTGGGTA 3180
Qy 3181 GAATTAACATCAATTTCCCAATCTTGAATTTGAGATGCTGTTATTTAGTATGAG 3240
Db 3181 GAATTAACATCAATTTCCCAATCTTGAATTTGAGATGCTGTTATTTAGTATGAG 3240
Qy 3241 GATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
Db 3241 GATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
Qy 3301 TGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3360
Db 3301 TGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3360
Qy 3361 CTCTG 3365
Db 3361 CTCTG 3365

RESULT 5
AEA36113

ID AEA36113 standard; DNA; 3380 BP.
 XX AEA36113;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Human nucleic acid sequence #45.
 XX
 KW Screening; gene expression; colorectal tumor; colitis; Crohn's disease;
 KM irritable bowel syndrome; gastrointestinal disease; cytostatic;
 KM gastrointestinal-gen.; antiinflammatory; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2005054507-A2.
 XX
 PD 16-JUN-2005.
 XX
 PF 03-DEC-2004; 2004WO-GB005078.
 XX
 PR 04-DEC-2003; 2003GB-00028048.
 XX
 PA (USH-) UNIV SHEPHERD.
 XX
 PI Corfe B, Chirakkal H;
 XX
 DR WPI; 2005-435407/44.
 XX
 PT Screening for nucleic acid molecules exhibiting altered expression in
 PT cells grown in the presence of butyrate, and detection of the nucleic
 PT acid molecules or the encoded polypeptides in diagnosing colorectal
 PT cancer.
 PS
 PS Disclosure; Page 77-78; 266pp; English.

CC irritable bowel syndrome, as a screening tool for fiber consumption, as
 CC an assay for colon microflora functionality or for early detection of pre
 CC -cancerous growth. This sequence represents a human nucleic acid
 CC identified by the screening method of the invention.
 XX
 SQ Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;
 Query Match 100.0%; Score 3365; DB 14; Length 3380;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCGCGGCGCTGAGAGCCCTGTGACAACTCGTCAATTGTGAGCAGACGGGTAGAC 60
 DB 1 GGGCGCGGCGCTGAGAGCCCTGTGACAACTCGTCAATTGTGAGCAGACGGGTAGAC 60
 QY 61 CCTGCTTCTCTAAGTGGGAGCGGAGCAGGCGCAGCAGCATTTCACTGTCCCGCAGACAA 120
 DB 61 CCTGCTTCTCTAAGTGGGAGCGGAGCAGGCGCAGCAGCATTTCACTGTCCCGCAGACAA 120
 QY 121 GAGCAGCATCTGCTTGGAGAACTCTTCCCTCTCTGAGAAAGAAAGTGTGAATGGG 180
 DB 121 GAGCAGCATCTGCTTGGAGAACTCTTCCCTCTCTGAGAAAGAAAGTGTGAATGGG 180
 QY 181 TATTCACAGAGAGAAATTTCCGCTATCTCATCTGTGCTTGAAGGCCAGGGTGAATAAG 240
 DB 181 TATTCACAGAGAGAAATTTCCGCTATCTCATCTGTGCTTGAAGGCCAGGGTGAATAAG 240
 QY 241 TACATCAGAGTGGAGCTGTGTGACTACCTGACCTTCTCTGAGAGGTGAAGAG 300
 DB 241 TACATCAGAGTGGAGCTGTGTGACTACCTGACCTTCTCTGAGAGGTGAAGAG 300
 QY 301 CAGATTGAGAGGAGAGTGGCCACCTCCGAGAAATGACAGCATTTGAACTGCTGTGAC 360
 DB 301 CAGATTGAGAGGAGAGTGGCCACCTCCGAGAAATGACAGCATTTGAACTGCTGTGAC 360
 QY 361 ACCTTGAGAGAGGAGTCTGGACCTTGTGATCTCGGGAATTTGTGAGGCCCTCCG 420
 DB 361 ACCTTGAGAGAGGAGTCTGGACCTTGTGATCTCGGGAATTTGTGAGGCCCTCCG 420
 QY 421 AGACCGGAGCGCTCTGGCCGCGCGCTACATGAACCTGAGCTCAGGACTTGGCCCT 480
 DB 421 AGACCGGAGCGCTCTGGCCGCGCGCTACATGAACCTGAGCTCAGGACTTGGCCCT 480
 QY 481 CCATGCTTTGAGAACGCTCATGATGATATTCCTCAACTGCTGACCTCTTCAAGCCACT 540
 DB 481 CCATGCTTTGAGAACGCTCATGATGATATTCCTCAACTGCTGACCTCTTCAAGCCACT 540
 QY 541 CTGGTGGACAACTTCTAGTTAGACGCTTGTGATTAAGTGAATGAGAGGAACTGTTG 600
 DB 541 CTGGTGGACAACTTCTAGTTAGACGCTTGTGATTAAGTGAATGAGAGGAACTGTTG 600
 QY 601 ACAATTGAAAGACAGAAACCGGATGCTGCTGAGAAAACATGGAATGAATCAGGTGA 660
 DB 601 ACAATTGAAAGACAGAAACCGGATGCTGCTGAGAAAACATGGAATGAATCAGGTGA 660
 QY 661 AGAGAGCTACTAAAAAGATTGTGAGAAAGAAAATGCTGCTGCAATTTTGAATGTT 720
 DB 661 AGAGAGCTACTAAAAAGATTGTGAGAAAGAAAATGCTGCTGCAATTTTGAATGTT 720
 QY 721 CTTTGTCAACGAGAAACATATACTTGTCCAAAGTTTAACGCTCTGATTTGCTCAGAA 780
 DB 721 CTTTGTCAACGAGAAACATATACTTGTCCAAAGTTTAACGCTCTGATTTGCTCAGAA 780
 QY 781 AGCAATGACAGATTGAGAAATTTATCACAAAGTTGATGCTCAAGTGAAGAGCACTT 840
 DB 781 AGCAATGACAGATTGAGAAATTTATCACAAAGTTGATGCTCAAGTGAAGAGCACTT 840
 QY 841 CTTTCAACCAAGTTCAGCCAAATCTGAGAAAGAGTGTGGGAGATGAGAAATTACTCA 900
 DB 841 CTTTCAACCAAGTTCAGCCAAATCTGAGAAAGAGTGTGGGAGATGAGAAATTACTCA 900
 QY 901 TGAAGATCATCTTTTGCAGATTCTTGTGAGTTTCAAGATCAGACAAAGTTTGGCAGAA 960
 DB 901 TGAAGATCATCTTTTGCAGATTCTTGTGAGTTTCAAGATCAGACAAAGTTTGGCAGAA 960

Db 901 TCAAGATCATCTTTGCAAGTTCTTGTAGTTTCAGAAATCAGACACAAAGTTGSCAGAA 960
Qy 961 GGAAGTGCAGCTGCTTAGATGAAGTCTTGACATACAGCAACATGGGCAAGTGAATCA 1020
Db 961 GGAAGTGCAGCTGCTTAGATGAAGTCTTGACATACAGCAACATGGGCAAGTGAATCA 1020
Qy 1021 GGCACCATGGGAAGTGAATCAGATGAAGAAATGTGGCAGCAAGACATCCCGGAGCCA 1080
Db 1021 GGCACCATGGGAAGTGAATCAGATGAAGAAATGTGGCAGCAAGACATCCCGGAGCCA 1080
Qy 1081 GAATCCAGCTCAGGCTTACCAAAATGGAAGTTGCCAGCCGCTTGAAAGGAAGAT 1140
Db 1081 GAATCCAGCTCAGGCTTACCAAAATGGAAGTTGCCAGCCGCTTGAAAGGAAGAT 1140
Qy 1141 ATCATCATCTGCTCCCTACAGGAGTGAAGAAACAGAGTGGCTTTTACATTGGCAAG 1200
Db 1141 ATCATCATCTGCTCCCTACAGGAGTGAAGAAACAGAGTGGCTTTTACATTGGCAAG 1200
Qy 1201 GATCACTTAGACAAAGAAAGAAAGCATCTGAGCTGGAAGAAAGTTAGTTCTTGTCAAT 1260
Db 1201 GATCACTTAGACAAAGAAAGAAAGCATCTGAGCTGGAAGAAAGTTAGTTCTTGTCAAT 1260
Qy 1261 AAGGTAATCTGTAGTGAACAGCTCTCCGCAAGAGATTCACATTTTGAAGAAATG 1320
Db 1261 AAGGTAATCTGTAGTGAACAGCTCTCCGCAAGAGATTCACATTTTGAAGAAATG 1320
Qy 1321 TATCGTGTATTGAGTTAAGTGGTGAATCCCACTGAATAATCATTTCCAGAAAGTTGTC 1380
Db 1321 TATCGTGTATTGAGTTAAGTGGTGAATCCCACTGAATAATCATTTCCAGAAAGTTGTC 1380
Qy 1381 AAGTCCGTGATATTTATTAATCAGTACAGCTCAAAATCCTTGAAATCCTCTTAACTTG 1440
Db 1381 AAGTCCGTGATATTTATTAATCAGTACAGCTCAAAATCCTTGAAATCCTCTTAACTTG 1440
Qy 1441 GAAATGGAAGAGATCTGTGTTCAATTGTCAAGATTTTCCCTCATTAATCATTAATGA 1500
Db 1441 GAAATGGAAGAGATCTGTGTTCAATTGTCAAGATTTTCCCTCATTAATCATTAATGA 1500
Qy 1501 TGTCAATCAGACCAAGAAAGAGAGATTAATTAATCATGAGGATTAATTTGATGAG 1560
Db 1501 TGTCAATCAGACCAAGAAAGAGAGATTAATTAATCATGAGGATTAATTTGATGAG 1560
Qy 1561 AAGTGAAGAAACAAATAGACTCAAGAAAGAAACAAACCAAGTATTCCTCTCAGATA 1620
Db 1561 AAGTGAAGAAACAAATAGACTCAAGAAAGAAACAAACCAAGTATTCCTCTCAGATA 1620
Qy 1621 CTGGGACTACAGCTTACCTGTGTTGAGAGGGGCCACGAGAGCAAGCCAAAGCTGAAGA 1680
Db 1621 CTGGGACTACAGCTTACCTGTGTTGAGAGGGGCCACGAGAGCAAGCCAAAGCTGAAGA 1680
Qy 1681 CACATTTTAAACTATGTGCCAATCTTGATGCAATTAATTAATCTGTAAAGAAAC 1740
Db 1681 CACATTTTAAACTATGTGCCAATCTTGATGCAATTAATTAATCTGTAAAGAAAC 1740
Qy 1741 CTTGATCACTGAAAAACCAATACAGAGCCATGCAAGAAAGTTGCCATTCAGATGA 1800
Db 1741 CTTGATCACTGAAAAACCAATACAGAGCCATGCAAGAAAGTTGCCATTCAGATGA 1800
Qy 1801 ACCAGAGAGATTCATTTAAGAAACTTCTAGAAATATGACAGATTCAAACTTAT 1860
Db 1801 ACCAGAGAGATTCATTTAAGAAACTTCTAGAAATATGACAGATTCAAACTTAT 1860
Qy 1861 TGTCAATGAGTGCATATGTCAGATTTTGGACATCAACCTATGACAAATGGGCAATTCA 1920
Db 1861 TGTCAATGAGTGCATATGTCAGATTTTGGACATCAACCTATGACAAATGGGCAATTCA 1920
Qy 1921 ATGGAAGAAAGCTGCAAAAGAAAGAAATGCAAGAAAGCTGTGTTGTCAGAACTTTG 1980
Db 1921 ATGGAAGAAAGCTGCAAAAGAAAGAAATGCAAGAAAGCTGTGTTGTCAGAACTTTG 1980
Qy 1981 AGGAAGTACAAATGAGGCTCTACAAATTAATGACAAATTCGAATGATGATGCGTATACT 2040
Db 1981 AGGAAGTACAAATGAGGCTCTACAAATTAATGACAAATTCGAATGATGATGCGTATACT 2040

Qy 2041 CATCTTGAAACTTTCTATATGAGAGAAAGATTAAGAACTTTCAGTCAATGAGATGAT 2100
Db 2041 CATCTTGAAACTTTCTATATGAGAGAAAGATTAAGAACTTTCAGTCAATGAGATGAT 2100
Qy 2101 AGTGAATGAGGCTGATGATGATATTTGTGATGTTGATGAGAAATGAGATGATTTAAG 2160
Db 2101 AGTGAATGAGGCTGATGATGATATTTGTGATGTTGATGAGAAATGAGATGATTTAAG 2160
Qy 2161 AAACCTTGAACTGATGATGAAACAGATGATTTCTCATGACTTTATTTTGAAGCAAT 2220
Db 2161 AAACCTTGAACTGATGATGAAACAGATGATTTCTCATGACTTTATTTTGAAGCAAT 2220
Qy 2221 AAAATGTTGAAAGCTGTGCTGAAAAACCAAGAAATGAAATGAAAGCTGACCAATTA 2280
Db 2221 AAAATGTTGAAAGCTGTGCTGAAAAACCAAGAAATGAAATGAAAGCTGACCAATTA 2280
Qy 2281 AGAATATCCATATGAGCAATATCTAGAGATGAGAAATCAGCAGAGAAATATCTTT 2340
Db 2281 AGAATATCCATATGAGCAATATCTAGAGATGAGAAATCAGCAGAGAAATATCTTT 2340
Qy 2341 ACAAACACGACAGATGATATGCGCTTCCAGTGGATTAAGTGAATGAAATTT 2400
Db 2341 ACAAACACGACAGATGATATGCGCTTCCAGTGGATTAAGTGAATGAAATTT 2400
Qy 2401 GCTGAAGTGAAGTCAAAAGCCACCATCTGATTTGAGCTGACACAGCAGTGAATCAAA 2460
Db 2401 GCTGAAGTGAAGTCAAAAGCCACCATCTGATTTGAGAGCTGACACAGCAGTGAATCAAA 2460
Qy 2461 CCCATGACACAGAAATGAACAAAAGAGTCAATTAATTTGCACTGGAAGAAATCAAT 2520
Db 2461 CCCATGACACAGAAATGAACAAAAGAGTCAATTAATTTGCACTGGAAGAAATCAAT 2520
Qy 2521 CTGCTTATGCTACACAGTGGCAGAAAGGCTGGAATTAAGAAATGTAACATGTT 2580
Db 2521 CTGCTTATGCTACACAGTGGCAGAAAGGCTGGAATTAAGAAATGTAACATGTT 2580
Qy 2581 ATCCGTTATGCTCTGCTCAACAATGAATAGCATGCTCAGAGCCGCTGAGGACAGA 2640
Db 2581 ATCCGTTATGCTCTGCTCAACAATGAATAGCATGCTCAGAGCCGCTGAGGACAGA 2640
Qy 2641 GCTGATGAGACACCTACGCTCTGTTGCTCAAGTGTTCAGAGTTATGCAATGAG 2700
Db 2641 GCTGATGAGACACCTACGCTCTGTTGCTCAAGTGTTCAGAGTTATGCAATGAG 2700
Qy 2701 ACAGTTATGATTTCCGAGAGAAATGATGATTAAGCTATACATTTGCTTCAAAATAG 2760
Db 2701 ACAGTTATGATTTCCGAGAGAAATGATGATTAAGCTATACATTTGCTTCAAAATAG 2760
Qy 2761 AAACAGAGAGATATGCTCATAGATTTTGAATTAACAGATGCAAAAGTAAATGAAAG 2820
Db 2761 AAACAGAGAGATATGCTCATAGATTTTGAATTAACAGATGCAAAAGTAAATGAAAG 2820
Qy 2821 AAAATGAAACCAAGAGAAATATTCGACAGATTAACAGAAATPACCATCAATTAAT 2880
Db 2821 AAAATGAAACCAAGAGAAATATTCGACAGATTAACAGAAATPACCATCAATTAAT 2880
Qy 2881 TTTCTTTGCAAAAACCTGAGTGTGCTAGCTGTTCTGGGGAAGATATCATGTAATGAG 2940
Db 2881 TTTCTTTGCAAAAACCTGAGTGTGCTAGCTGTTCTGGGGAAGATATCATGTAATGAG 2940
Qy 2941 AAAATGCAATCAGTCAATATGACCCGACAGAACTTCAAGAACTTACATGTAAGAGAAAC 3000
Db 2941 AAAATGCAATCAGTCAATATGACCCGACAGAACTTCAAGAACTTACATGTAAGAGAAAC 3000
Qy 3001 AAAGCATCTGCAAAAGAGTGTCCGACTATCAATTAATGTAATCAATCTGCAATGT 3060
Db 3001 AAAGCATCTGCAAAAGAGTGTCCGACTATCAATTAATGTAATCAATCTGCAATGT 3060
Qy 3061 GGCAGGCTTGGGGAACAATGATGTCACAAAGCTTATGATTTGCTTGTCTCAAAATA 3120
Db 3061 GGCAGGCTTGGGGAACAATGATGTCACAAAGCTTATGATTTGCTTGTCTCAAAATA 3120

QY 3121 AGGAATTTGTAGTGGTTTCAAAAATATTCACAAGAAACATACAAAAAGTGGTA 3180
| | | | |
DB 3121 AGGAATTTGTAGTGGTTTCAAAAATATTCACAAGAAACATACAAAAAGTGGTA 3180
| | | | |
QY 3181 GAATTAACCTACACATTTCCCAATCTGACTATTCAGAAATGCGTTATTTAGTGTAG 3240
| | | | |
DB 3181 GAATTAACCTACACATTTCCCAATCTGACTATTCAGAAATGCGTTATTTAGTGTAG 3240
| | | | |
QY 3241 GATTAGCACTGATTGAGATTTCTTTAAATACATATCAGTTAAACATTTAATATGATTA 3300
| | | | |
DB 3241 GATTAGCACTGATTGAGATTTCTTTAAATACATATCAGTTAAACATTTAATATGATTA 3300
| | | | |
QY 3301 TGATTAATGATTATTCATTAATGCTACAGAACTGACATATGAAATGATTTGTTTA 3360
| | | | |
DB 3301 TGATTAATGATTATTCATTAATGCTACAGAACTGACATATGAAATGATTTGTTTA 3360
| | | | |
QY 3361 CTCTG 3365
| | | | |
DB 3361 CTCTG 3365
| | | | |

RESULT 6

ADY17563
ID ADY17563 standard; DNA: 3434 BP.

ADY17563;
XX

05-MAY-2005 (first entry)
XX

DE DNA encoding a PRO polypeptide, SEQ ID NO 3369.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Vincicid; Gastrointestinal-Gen.; Antipneumatic; Antiasmatic;
XX Antiallergic; ds; gene; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 1; SEQ ID NO 3369; 158bp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 3434 BP; 1157 A; 673 C; 768 G; 836 T; 0 U; 0 Other;

XX Query Match 99.9%; Score 3361.8; DB 14; Length 3434;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 3363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCGCGGCTTGAAGCCCTGTGACACACTTGTCTATTGTGAGCAGAGCGGTAGAC 60
| | | | |

DB 55 GCGCGCGGCTTGAAGCCCTGTGACACACTTGTCTATTGTGAGCAGAGCGGTAGAC 114
| | | | |
QY 61 CCTGCTTCTTAAGTGGGCAAGGCAAGGCGGACGCACTTCCCTGCGGACAA 120
| | | | |
DB 115 CCTGCTTCTTAAGTGGGCAAGGCAAGGCGGACGCACTTCCCTGCGGACAA 174
| | | | |
QY 121 CAGCAACATCTGCTGGGGAACCTTCCCTCTGAGAAAGAAATGCGATGGG 180
| | | | |
DB 175 CAGCAACATCTGCTGGGGAACCTTCCCTCTGAGAAAGAAATGCGATGGG 234
| | | | |
QY 181 TATTCCACAGAGAAATTTCCGCTATCTCATCTGCTGAGGGCCAGGTGAAAATG 240
| | | | |
DB 235 TATTCCACAGAGAAATTTCCGCTATCTCATCTGCTGAGGGCCAGGTGAAAATG 294
| | | | |
QY 241 TACATCCAGGTGAGCTGTGTGGAATACCTGACCTTTCTGCTGAGAGGTGAAGAG 300
| | | | |
DB 295 TACATCCAGGTGAGCTGTGTGGAATACCTGACCTTTCTGCTGAGAGGTGAAGAG 354
| | | | |
QY 301 CAGATTCAGAGACAGTGGCCACTTCCGGGAACATGCAAGGCAATTGACTGCTGAGC 360
| | | | |
DB 355 CAGATTCAGAGACAGTGGCCACTTCCGGGAACATGCAAGGCAATTGACTGCTGAGC 414
| | | | |
QY 361 ACCTTGAGAGAGAGTCTGGCACTTGGTGGACTCGGGAAATTCGTGAGGCGCTCCGG 420
| | | | |
DB 415 ACCTTGAGAGAGAGTCTGGCACTTGGTGGACTCGGGAAATTCGTGAGGCGCTCCGG 474
| | | | |
QY 421 AGAACCGGAGCGCTCTGGCGCGCGCTACATGAACCTTGAGCTCAGGACTTCCCTCT 480
| | | | |
DB 475 AGAACCGGAGCGCTCTGGCGCGCGCTACATGAACCTTGAGCTCAGGACTTCCCTCT 534
| | | | |
QY 481 CCATGCTTGAAGACGCTCATATGAAATCTCCAACTGCTGAACCTCTTGAGCCACT 540
| | | | |
DB 535 CCATGCTTGAAGACGCTCATATGAAATCTCCAACTGCTGAACCTCTTGAGCCACT 594
| | | | |
QY 541 CTGCTGACAACTTCTAGTGAAGACGCTTGATGAGTGAAGTGAAGGAGAACTGTG 600
| | | | |
DB 595 CTGCTGACAACTTCTAGTGAAGACGCTTGATGAGTGAAGTGAAGGAGAACTGTG 654
| | | | |
QY 601 ACAATTTGAAGACAGAAACCGATTCGCTGAGAAACATGAAATGAATCAAGTGA 660
| | | | |
DB 655 ACAATTTGAAGACAGAAACCGATTCGCTGAGAAACATGAAATGAATCAAGTGA 714
| | | | |
QY 661 AGAGAGCTACTAAAAAGATTTGTGCAAGAAAGAACTGGTTCTTCGCAATTTCTGAATGT 720
| | | | |
DB 715 AGAGAGCTACTAAAAAGATTTGTGCAAGAAAGAACTGGTTCTTCGCAATTTCTGAATGT 774
| | | | |
QY 721 CTTTGTCAACAGAGAAACAAATGAATCTTCCAAAGATTAAACAGGCTCTGATTCAGAA 780
| | | | |
DB 775 CTTTGTCAACAGAGAAACAAATGAATCTTCCAAAGATTAAACAGGCTCTGATTCAGAA 834
| | | | |
QY 781 AGCAATGCAGAGATTGAGAAATTTATCACAAGTTGATGCTCAAGTGAAGAGCAACT 840
| | | | |
DB 835 AGCAATGCAGAGATTGAGAAATTTATCACAAGTTGATGCTCAAGTGAAGAGCAACT 894
| | | | |
QY 841 CTTTCAACACAGCTTCAAGCAAAATGTGGAAGAGAGTGTGGGCAATGAGAAATACTCA 900
| | | | |
DB 895 CTTTCAACACAGCTTCAAGCAAAATGTGGAAGAGAGTGTGGGCAATGAGAAATACTCA 954
| | | | |
QY 901 TCAGATATCATCTTTGACAGATTCTTCTGATTTGAGATTCAGATTCAGACACAGATTGGCAGAA 960
| | | | |
DB 955 TCAGATATCATCTTTGACAGATTCTTCTGATTTGAGATTCAGATTCAGACACAGATTGGCAGAA 1014
| | | | |
QY 961 GGAAGTGCAGTCTTATGATGAAAGCTTTGACATTAACAGCAACATGGGCAAGTATTC 1020
| | | | |
DB 1015 GGAAGTGCAGTCTTATGATGAAAGCTTTGACATTAACAGCAACATGGGCAAGTATTC 1074
| | | | |
QY 1021 GGCACCATGGGAAGTGAATTCAGATGAAGAAATGTGGCAGCAAGCATCCCGGAGCCA 1080
| | | | |
DB 1075 GGCACCATGGGAAGTGAATTCAGATGAAGAAATGTGGCAGCAAGCATCCCGGAGCCA 1134
| | | | |
QY 1081 GAACTCAGCTCAGGCTTAACCAAAATGGAAGTTGGCCAGCCCTTGAAGAGGAAGAT 1140
| | | | |
DB 1135 GAACTCAGCTCAGGCTTAACCAAAATGGAAGTTGGCCAGCCCTTGAAGAGGAAGAT 1194
| | | | |

QY 1141 ATCATCATCTGCTCCCTACAGGAGTGGAAAAACCAAGTGTGCTGTTACATTGCGAAG 1200
DB 1195 ATCATCATCTGCTCCCTACAGGAGTGGAAAAACCAAGTGTGCTGTTACATTGCGAAG 1254
QY 1201 GATCCTTAGACAAGAAAAAAGCATCTGAGCCGTGAAAAAGTTATAGTCTGTGCAT 1260
DB 1255 GATCCTTAGACAAGAAAAAAGCATCTGAGCCGTGAAAAAGTTATAGTCTGTGCAT 1314
QY 1261 AAGTACTGCTAGTGAAGAGCTCTCCGCAAGAGTCCAAACATTTTGAAGAAATG 1320
DB 1315 AAGTACTGCTAGTGAAGAGCTCTCCGCAAGAGTCCAAACATTTTGAAGAAATG 1374
QY 1321 TATCGTATTAGATTAAAGTGTGATACCACTGAAAAATATCATTTCCAGAGTTGTC 1380
DB 1375 TATCGTATTAGATTAAAGTGTGATACCACTGAAAAATATCATTTCCAGAGTTGTC 1434
QY 1381 AAGTCTGTGATATTATTATCAGTACAGTCAAACTCTGAAAACTCCCTTTAAACTTG 1440
DB 1435 AAGTCTGTGATATTATTATCAGTACAGTCAAACTCTGAAAACTCCCTTTAAACTTG 1494
QY 1441 GAAAAATGAGAAAGATGCTGCTGTTCAATTGTGAGACTTTTCCCTCATATCATGATGA 1500
DB 1495 GAAAAATGAGAAAGATGCTGCTGTTCAATTGTGAGACTTTTCCCTCATATCATGATGA 1554
QY 1501 TGTCAATCACCAACCAAGAGAGTGTATTAATATCATGATGAGGATTTATTTGATGAG 1560
DB 1555 TGTCAATCACCAACCAAGAGAGTGTATTAATATCATGATGAGGATTTATTTGATGAG 1614
QY 1561 AAGTTGAAAAACATATGACTCAAGAAAAAACAACAGTATTCCTCTCTCAGATA 1620
DB 1615 AAGTTGAAAAACATATGACTCAAGAAAAAACAACAGTATTCCTCTCTCAGATA 1674
QY 1621 CTGGGACTAAGCTTCACTGTGTGTGAGGGGGCCACGAGAGAGCCAAAGCTGAAGA 1680
DB 1675 CTGGGACTAAGCTTCACTGTGTGTGAGGGGGCCACGAGAGAGCCAAAGCTGAAGA 1734
QY 1681 CACATTTTAAAACTATGTGCCAATCTTGATGCAATTTACTATTAAACGTGTAAGAAAC 1740
DB 1735 CACATTTTAAAACTATGTGCCAATCTTGATGCAATTTACTATTAAACGTGTAAGAAAC 1794
QY 1741 CTTGATCAACTGAAAAACCAATATACGAGGCCATGCAAGAGTTGGCCATTGCAATGCA 1800
DB 1795 CTTGATCAACTGAAAAACCAATATACGAGGCCATGCAAGAGTTGGCCATTGCAATGCA 1854
QY 1801 ACCAGGAAGATCCATTTAAAGAAACCTTCTAGAAATATGACAAAGATTCGAACCTTAT 1860
DB 1855 ACCAGGAAGATCCATTTAAAGAAACCTTCTAGAAATATGACAAAGATTCGAACCTTAT 1914
QY 1861 TGTCAATAGTCCAAATGTCAATTTTGGAACTCAACCCCTATGAACATGGGCCATTGCA 1920
DB 1915 TGTCAATAGTCCAAATGTCAATTTTGGAACTCAACCCCTATGAACATGGGCCATTGCA 1974
QY 1921 ATGAAAAAAGAGCTGCAAAAAAAGAAATGCAAAAGAAAGTGTGTCAGAAACATTTG 1980
DB 1975 ATGAAAAAAGAGCTGCAAAAAAAGAAATGCAAAAGAAAGTGTGTCAGAAACATTTG 2034
QY 1981 AGGAAGTACAAATGAGGCCCTACAAATTAATGACAAATTCGAATGATATATGCTATCT 2040
DB 2035 AGGAAGTACAAATGAGGCCCTACAAATTAATGACAAATTCGAATGATATATGCTATCT 2094
QY 2041 CATCTTGAACCTTTCTATATATGAGAAAGAAATGAGAAATGCTGAGTCAATGAGTAT 2100
DB 2095 CATCTTGAACCTTTCTATATATGAGAAAGAAATGAGAAATGCTGAGTCAATGAGTAT 2154
QY 2101 AGTGAATGAGGGTGTGATGATGATATTTGTGATGATGATGATGATGATGATGATGAT 2160
DB 2155 AGTGAATGAGGGTGTGATGATGATATTTGTGATGATGATGATGATGATGATGATGAT 2214
QY 2161 AAACTTTGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
DB 2215 AAACTTTGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2274

QY 2221 AAAATGTTGAAAGGCTGCTGAAAAACCAAGATTAAGAAAAATGAAAAAGTGAACCAATTA 2280
DB 2275 AAAATGTTGAAAGGCTGCTGAAAAACCAAGATTAAGAAAAATGAAAAAGTGAACCAATTA 2334
QY 2281 AGAAATACCAATATGAGAGCAATATCTAGAGCTGAGAAATGACGACGAGAAATATCTTT 2340
DB 2335 AGAAATACCAATATGAGAGCAATATCTAGAGCTGAGAAATGACGACGAGAAATATCTTT 2394
QY 2341 AAAAAAACAACAAGAGTGCATATGCGCTTTCCAGTGGATTAAGTAAAAATGAAAAATTT 2400
DB 2395 AAAAAAACAACAAGAGTGCATATGCGCTTTCCAGTGGATTAAGTAAAAATGAAAAATTT 2454
QY 2401 GCTGAATGAGAGTCAAAAGCCCACTGATGATGAGCTGCAACAAGAGTGAATTTGAA 2460
DB 2455 GCTGAATGAGAGTCAAAAGCCCACTGATGATGAGCTGCAACAAGAGTGAATTTGAA 2514
QY 2461 CCCATGACACAAATGAACAAAAAAGCTATTAATTTGCACTGGAATAATCAAT 2520
DB 2515 CCCATGACACAAATGAACAAAAAAGCTATTAATTTGCACTGGAATAATCAAT 2574
QY 2521 CTGCTTATCGTACCAAGAGTGCAGAGAGGCTGATATTAAGAAATGTAACATTTGT 2580
DB 2575 CTGCTTATCGTACCAAGAGTGCAGAGAGGCTGATATTAAGAAATGTAACATTTGT 2634
QY 2581 ATCGGTTATGCTCTGTCACCAATGAATAGCCATGCTCAGGCCCTGCTGAGCCAGA 2640
DB 2635 ATCGGTTATGCTCTGTCACCAATGAATAGCCATGCTCAGGCCCTGCTGAGCCAGA 2694
QY 2641 GCTGATGAGAGCACTTACGTCTGTGTGCTCAGTGTGTCAGAGTTATGCAACATGAG 2700
DB 2695 GCTGATGAGAGCACTTACGTCTGTGTGCTCAGTGTGTCAGAGTTATGCAACATGAG 2754
QY 2701 ACAGTTAATGATTTCCGAGAGAAAGATGATGATTAAGCTATCATTTGTCAAAATATG 2760
DB 2755 ACAGTTAATGATTTCCGAGAGAAAGATGATGATTAAGCTATCATTTGTCAAAATATG 2814
QY 2761 AAACCAAGAGATGCTCATATGATTTTGAATTAACAGATCAAGTCAAAATGTAAGAAAG 2820
DB 2815 AAACCAAGAGATGCTCATATGATTTTGAATTAACAGATCAAGTCAAAATGTAAGAAAG 2874
QY 2821 AAAATGAAAAACCAAGAAATTTTGGCAAGCTTCAAGAAATACCCATCATATTAAT 2880
DB 2875 AAAATGAAAAACCAAGAAATTTTGGCAAGCTTCAAGAAATACCCATCATATTAAT 2934
QY 2881 TTCCTTGCAAAACTGCAAGTGTGCTAGCTGTTCTGGGGAAATATCATGTAATTTGAG 2940
DB 2935 TTCCTTGCAAAACTGCAAGTGTGCTAGCTGTTCTGGGGAAATATCATGTAATTTGAG 2994
QY 2941 AAAATGCAATCAAGTCAATATGACCCAGAAATTCAGAGAACTTTACATTTGAAGAGAAAC 3000
DB 2995 AAAATGCAATCAAGTCAATATGACCCAGAAATTCAGAGAACTTTACATTTGAAGAGAAAC 3054
QY 3001 AAAGCACTGCAAAAGAGTGTGCCGATATCAATTAATGTTGAATCATCTGCAATGT 3060
DB 3055 AAAGCACTGCAAAAGAGTGTGCCGATATCAATTAATGTTGAATCATCTGCAATGT 3114
QY 3061 GGCCAGGCTGGGGGAAACAATATGTTGCAAAAGGCTTAGATTTGCTGCTCAAAATA 3120
DB 3115 GGCCAGGCTGGGGGAAACAATATGTTGCAAAAGGCTTAGATTTGCTGCTCAAAATA 3174
QY 3121 AGGAATTTTGTATGTTGTTTCAAAATATATTCACAAAGAAACAATATACAAAAAGTGGTA 3180
DB 3175 AGGAATTTTGTATGTTGTTTCAAAATATATTCACAAAGAAACAATATACAAAAAGTGGTA 3234
QY 3181 GAATTAACCTATCACTTTCCCAATCTGATATGAGATGCTGTTTATTTAGTATGAG 3240
DB 3235 GAATTAACCTATCACTTTCCCAATCTGATATGAGATGCTGTTTATTTAGTATGAG 3294
QY 3241 GATTAGCACTGATGAGATTTCTTTAAATATCATATGATGATTAATGATTAATGATTA 3300
DB 3295 GATTAGCACTGATGAGATTTCTTTAAATATCATATGATGATTAATGATTAATGATTA 3354
QY 3301 TGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 3360

Db 3355 TGAATTAATGATTCATTATGCTACAGAACTGACATGATAAGATCAATTAATGATTTGTTTA 3414
QY 3361 CTCTG 3365
Db 3415 CTCTG 3419

RESULT 7
ADY20376
ID ADY20376 standard; DNA; 3434 BP.
XX
AC ADY20376;
XX
DT 05-MAY-2005 (first entry)
XX
DE DNA encoding a PRO polypeptide, SEQ ID NO 6182.
XX
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Viricide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; ds; gene; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004WO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX
PA (GENTH) GEMENTECH INC.
XX
FI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX
DR WPI; 2005-182330/19.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 1; SEQ ID NO 6182; 1589P; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.
XX
SQ Sequence 3434 BP; 1157 A; 673 C; 768 G; 836 T; 0 U; 0 Other;

Query Match 99.9%; Score 3361.8; DB 14; Length 3434;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGCGCGCGCTGAGAGCCCTGTGACAACTCTGATTCAGAGACAGAGCGGTAGAC 60
Db 55 GGGCGCGCGCTGAGAGCCCTGTGACAACTCTGATTCAGAGACAGAGCGGTAGAC 114
QY 61 CCTGCTTCTTAAGTGGGAGCGGACAGGCGGACATTTCACTGTCCGACAGAA 120
Db 115 CCTGCTTCTTAAGTGGGAGCGGACAGGCGGACATTTCACTGTCCGACAGAA 174
QY 121 CAGACCAATCTGCTTGGGAGAACTCTCTCTTCTGTGAAAAGAAAGTGTGAATGG 180
Db 175 CAGACCAATCTGCTTGGGAGAACTCTCTCTTCTGTGAAAAGAAAGTGTGAATGG 234
QY 181 TATTCACAGAGAAATTTCCGCTATTCATCTCGTGTTCAGGGCCAGGGTGAATG 240
Db 235 TATTCACAGAGAAATTTCCGCTATTCATCTCGTGTTCAGGGCCAGGGTGAATG 294

QY 241 TACATCCAGGTGAGACCTGTGTGATTAATCTGACCTTTTCCCTGACAGGTGAAGAG 300
Db 295 TACATCCAGGTGAGACCTGTGTGATTAATCTGACCTTTTCCCTGACAGGTGAAGAG 354
QY 301 CAGATTCAGAGACAGTCCGACCTCCGGGAAATGACAGAGTTGAATCTGCTGAGC 360
Db 355 CAGATTCAGAGACAGTCCGACCTCCGGGAAATGACAGAGTTGAATCTGCTGAGC 414
QY 361 ACCTTGAGAAAGGAGTGTGCACTTGTGTGACTCGGAAATTTGTGAGGCGCTCCGG 420
Db 415 ACCTTGAGAAAGGAGTGTGCACTTGTGTGACTCGGAAATTTGTGAGGCGCTCCGG 474
QY 421 AGAACGGGACGCGCTCTGCGCGCGCGCTTACATGAACCTTGAGCTACAGGACTTGGCCT 480
Db 475 AGAACGGGACGCGCTCTGCGCGCGCGCTTACATGAACCTTGAGCTACAGGACTTGGCCT 534
QY 481 CCATGTTTGAAGACGCTCATGATGATATCTCCAACTGTGAACTCTTCAGGCCACT 540
Db 535 CCATGTTTGAAGACGCTCATGATGATATCTCCAACTGTGAACTCTTCAGGCCACT 594
QY 541 CTGATGACAAAGCTTCTAGTTAGAGACGCTTGTGATTAAGTCATGAGAGAGAACTGTG 600
Db 595 CTGATGACAAAGCTTCTAGTTAGAGACGCTTGTGATTAAGTCATGAGAGAGAACTGTG 654
QY 601 ACAATTGAAGACAGAAACCGGATTCCTGTCAGAAAAATGAAATGAATCAGGTGA 660
Db 655 ACAATTGAAGACAGAAACCGGATTCCTGTCAGAAAAATGAAATGAATCAGGTGA 714
QY 661 AGAGAGCTAATAAAGATTTGTGCAAGAAAGAACTGGTCTCTGCAATTCGAAATGT 720
Db 715 AGAGAGCTAATAAAGATTTGTGCAAGAAAGAACTGGTCTCTGCAATTCGAAATGT 774
QY 721 CTTGCTCAACAGGAAACATGAATCTGTCCAGAGATTACAGGCTCTGATTTGCTCAGAA 780
Db 775 CTTGCTCAACAGGAAACATGAATCTGTCCAGAGATTACAGGCTCTGATTTGCTCAGAA 834
QY 781 AGCAATGACAGAGATTGAAGATTTATCACAAGTTGATGCTCCTCAAGTGAAGACAACT 840
Db 835 AGCAATGACAGAGATTGAAGATTTATCACAAGTTGATGCTCCTCAAGTGAAGACAACT 894
QY 841 CTTTCAACACAGTTCAGGCAATCTGAGAAAGAGCTGCGGAGCATGAGAAATTAATCA 900
Db 895 CTTTCAACACAGTTCAGGCAATCTGAGAAAGAGCTGCGGAGCATGAGAAATTAATCA 954
QY 901 TCAGATCATCTTTTTCAGATTTCTTGTAGTTTCAGATTCAGACACAAAGTTTGGCAGAA 960
Db 955 TCAGATCATCTTTTTCAGATTTCTTGTAGTTTCAGATTCAGACACAAAGTTTGGCAGAA 1014
QY 961 GGAAGTGTGAGCTGCTTGAATGAAGAGCTTGGACATTAACAGCAATAGGGCAGTATTC 1020
Db 1015 GGAAGTGTGAGCTGCTTGAATGAAGAGCTTGGACATTAACAGCAATAGGGCAGTATTC 1074
QY 1021 GGCACCAATGGGAGATTTTCAGATGAAGAGATGTGGACAGAAAGCAATCCCGGAGCA 1080
Db 1075 GGCACCAATGGGAGATTTTCAGATGAAGAGATGTGGACAGAAAGCAATCCCGGAGCA 1134
QY 1081 GAATCTCAGAGCTTACCAATGGAAGTTGCCAGCCAGCCTTGGAAAGGAAGAT 1140
Db 1135 GAATCTCAGAGCTTACCAATGGAAGTTGCCAGCCAGCCTTGGAAAGGAAGAT 1194
QY 1141 ATCATCATCTGCTCTTACAGGAGGTGAAACCAAGATGAGCTGTTTACATTGCCAAG 1200
Db 1195 ATCATCATCTGCTCTTACAGGAGGTGAAACCAAGATGAGCTGTTTACATTGCCAAG 1254
QY 1201 GATCATCTTAAGCAAAAGAAAGAAAGCACTGAGCCTGAGAAAGTATATGTTCTTGTCAAT 1260
Db 1255 GATCATCTTAAGCAAAAGAAAGAAAGCACTGAGCCTGAGAAAGTATATGTTCTTGTCAAT 1314
QY 1261 AAGGTACTGATGGAACAGCTCTTCGCAAGAGATTCCAACCAATTTTGAAGAAATGG 1320
Db 1315 AAGGTACTGATGGAACAGCTCTTCGCAAGAGATTCCAACCAATTTTGAAGAAATGG 1374

1321 TATCGTTATTTGGATTAAAGTGTGATACCAGCTGAAAAATATCATTTCAGAGATTGTC 1380
1375 TATCGTTATTTGGATTAAAGTGTGATACCAGCTGAAAAATATCATTTCAGAGATTGTC 1434
1381 AAGTCTGTGATTTATTTATTCAGTCAAGTCAATCTTGAAAACTCCCTTAACTTG 1440
1435 AAGTCTGTGATTTATTTATTCAGTCAAGTCAATCTTGAAAACTCCCTTAACTTG 1494
1441 GAAAAATGAGAAAGATCTGTGTTCAATTTGTGAGCTTTTCCCTCATTTATCATTTGATGA 1500
1495 GAAAAATGAGAAAGATCTGTGTTCAATTTGTGAGCTTTTCCCTCATTTATCATTTGATGA 1554
1501 TGTCAATCAACCAACCAAGAGAGTGTATTAATACATCAATGAGCATTTATTTGATGAG 1560
1555 TGTCAATCAACCAACCAAGAGAGTGTATTAATACATCAATGAGCATTTATTTGATGAG 1614
1561 AAGTTGAAAAATGATGATCTCAAGAAAGAAAAACCAACCAATGATTTCCCTTCTCGATGA 1620
1615 AAGTTGAAAAATGATGATCTCAAGAAAGAAAAACCAACCAATGATTTCCCTTCTCGATGA 1674
1621 CTGGAGCTAACAGCTTCACTGTGTGTTGAGGGGCCACGAGCAAGCAAGCTGAAGAA 1680
1675 CTGGAGCTAACAGCTTCACTGTGTGTTGAGGGGCCACGAGCAAGCAAGCTGAAGAA 1734
1681 CACATTTTAAACTATGTGCCAATCTTGATGCAATTTACTATTTAAACCTGTTAAAGAAAC 1740
1735 CACATTTTAAACTATGTGCCAATCTTGATGCAATTTACTATTTAAACCTGTTAAAGAAAC 1794
1741 CTTGATCAACTGAAAAACCAATATCAGAGAGCCATGCAAGAGTTTGCATTTGAGATGCA 1800
1795 CTTGATCAACTGAAAAACCAATATCAGAGAGCCATGCAAGAGTTTGCATTTGAGATGCA 1854
1801 ACCAGAGAGATCATTTTAAAGAGAACTCTGAAATATATGACAGAGATTCAACTTAT 1860
1855 ACCAGAGAGATCATTTTAAAGAGAACTCTGAAATATATGACAGAGATTCAACTTAT 1914
1861 TGTCAATGATGCTCAATGTGATTTGGAATCTCAACCTATGAAATGAGGCATTTCA 1920
1915 TGTCAATGATGCTCAATGTGATTTGGAATCTCAACCTATGAAATGAGGCATTTCA 1974
1921 ATGGAAGAAAAAGCTGCAAAAAAGAAATCGCAAGAACGTGTTGTGCAAACTTTG 1980
1975 ATGGAAGAAAAAGCTGCAAAAAAGAAATCGCAAGAACGTGTTGTGCAAACTTTG 2034
1981 AGGAATACAAATGAGGCCCTCAAAATTAATGACAAATTCGAATGATGATGCTATCT 2040
2035 AGGAATACAAATGAGGCCCTCAAAATTAATGACAAATTCGAATGATGATGCTATCT 2094
2041 CATCTTGAACCTTCTATATATGAGAGAAAGATTAAGATTGTCAGTCAATGAGATGAT 2100
2095 CATCTTGAACCTTCTATATATGAGAGAAAGATTAAGATTGTCAGTCAATGAGATGAT 2154
2101 AGTGAAGAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
2155 AGTGAAGAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2214
2161 AAAACCTTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2215 AAAACCTTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2274
2221 AAAATTTGAAAAAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2275 AAAATTTGAAAAAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2334
2281 AGAAATACCAATATGAGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
2335 AGAAATACCAATATGAGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2394
2341 AAAAAAACAACGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
2395 AAAAAAACAACGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2454
2401 GCTGAAGTGAAGTCAAAAGCCCAATCTGATTTGAGATGATGATGATGATGATGATGATGAT 2460

2455 GCTGAAGTGAAGTCAAAAGCCCAATCTGATTTGAGATGATGATGATGATGATGATGATGAT 2514
2461 CCCATGACACAGAAATGAACAAAAAGAGTCAATTAATTAATTTGCACTGAAAAATCAAT 2520
2515 CCCATGACACAGAAATGAACAAAAAGAGTCAATTAATTAATTTGCACTGAAAAATCAAT 2574
2521 CTGCTTATGCTTACCAACAGTGTGAGAGAGGTCTGATATTTAAAGATGTAACATTTGTT 2580
2575 CTGCTTATGCTTACCAACAGTGTGAGAGAGGTCTGATATTTAAAGATGTAACATTTGTT 2634
2581 ATCCGTTATGTTCTGTCTACCAATGAATATGATGATGATGATGATGATGATGATGATGATGAT 2640
2635 ATCCGTTATGTTCTGTCTACCAATGAATATGATGATGATGATGATGATGATGATGATGATGAT 2694
2641 GCTGAAGTGAAGTCAAAAGCCCAATCTGATTTGAGATGATGATGATGATGATGATGATGAT 2700
2695 GCTGAAGTGAAGTCAAAAGCCCAATCTGATTTGAGATGATGATGATGATGATGATGATGAT 2754
2701 ACAGTTAATGATTTTCCAGAGAGAGATGATGATTAAGCTATACTTTGTTCAAAATATG 2760
2755 ACAGTTAATGATTTTCCAGAGAGAGATGATGATTAAGCTATACTTTGTTCAAAATATG 2814
2761 AAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
2815 AAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2874
2821 AAATGAAAAACCAAGAGAAATTTGCAAGATTTTCAAGATTAACCAATCACTCAATTAATCT 2880
2875 AAATGAAAAACCAAGAGAAATTTGCAAGATTTTCAAGATTAACCAATCACTCAATTAATCT 2934
2881 TTCTTTGCAAAAACTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
2935 TTCTTTGCAAAAACTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2994
2941 AAATGATCACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
2995 AAATGATCACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3054
3001 AAAGCACTGCAAAAAAGAGTGTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3060
3055 AAAGCACTGCAAAAAAGAGTGTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3114
3061 GGCAGAGCTTGGAGGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3115 GGCAGAGCTTGGAGGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3174
3121 AGGAATTTTGTAGTGTGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3180
3175 AGGAATTTTGTAGTGTGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3234
3181 GAATTAATGATCAATTTTCCCAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 3240
3235 GAATTAATGATCAATTTTCCCAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 3294
3241 GATTAAGCACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
3295 GATTAAGCACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3354
3301 TGATTAATGATCAATTTTCCCAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3355 TGATTAATGATCAATTTTCCCAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 3414
3361 CTCTG 3365
3415 CTCTG 3419

RESULT 8
ACN91892
ID ACN91892 standard; DNA; 3928 BP.
XX
AC ACN91892;

XX 02-DEC-2004 (first entry)
XX Breast cancer related marker, seq id 13042.
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX Homo sapiens.
XX US2003099974-A1.
XX 29-MAY-2003.
XX 18-JUL-2002; 2002US-00198846.
XX 18-JUL-2001; 2001US-0306220P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2003-787014/74.
XX Novel isolated polypeptide associated with breast cancer, useful for
XX detecting presence of polypeptide in sample, as a marker for breast
XX cancer.
XX Disclosure; SEQ ID NO 13042; 36pp; English.
XX The invention relates to an isolated polypeptide (I) associated with
XX breast cancer which is encoded by a nucleic acid molecule comprising a
XX nucleotide sequence (S1). Further disclosed is an antibody that binds to
XX the polypeptide of the invention. The activity of the polypeptide of the
XX invention may be described as cytostatic. The antibody is useful for
XX detecting the presence of (I) in a sample. Nucleic acid molecules of the
XX invention are useful in the detection of breast tumours. (I) is useful as
XX a marker for breast cancer and in breast cancer therapy. Sequences given
XX in records ACN78851-ACN92934 represent nucleic acid markers associated
XX with breast cancer. Note: The sequence listing does not form part of the
XX specification but may be obtained in electronic format from the USPTO web
XX site at seqdata.uspto.gov/sequence.html?DocID=20030099974
SQ Sequence 3928 BP; 1285 A; 826 C; 895 G; 917 T; 0 U; 5 Other;
Query Match 99.9%; Score 3360.2; DB 11; Length 3928;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3362; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCGCGCCGCGCTGAGAGCCCTGTGACACCTGTCATTGTCAAGCAAGAGCGGTAGAC 60
DB 443 GCGCGCCGCGCTGAGAGCCCTGTGACACCTGTCATTGTGTAGGACAGAGCGGTAGAC 502
QY 61 CCGCTCTCTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 503 CCGCTCTCTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
QY 121 CAGCACCATCTGCTGGGAGAACCTCTCCCTTCTGTGAGAAAGAAAGATGTGAATGGG 180
DB 563 CAGCACCATCTGCTGGGAGAACCTCTCCCTTCTGTGAGAAAGAAAGATGTGAATGGG 622
QY 181 TATTCACAGACGAGATTTCCGCTATCTCATCTGCTTCAAGGCGCAGGAGTGAATG 240
DB 623 TATTCACAGACGAGATTTCCGCTATCTCATCTGCTTCAAGGCGCAGGAGTGAATG 682
QY 241 TACATCAGGTGAGAGCTGTGTGAGACTACCTTCTGCTGTGAGAGGTGAAGAG 300
DB 683 TACATCAGGTGAGAGCTGTGTGAGACTACCTTCTGCTGTGAGAGGTGAAGAG 742
QY 301 CAGATTCAAGAGCAGTCCGACCTCCGAGGACATGAGGAGGAGTGAATGCTGTAGC 360
DB 743 CAGATTCAAGAGCAGTCCGACCTCCGAGGACATGAGGAGGAGTGAATGCTGTAGC 802
QY 361 ACCTTGAGAGAGAGTGTGGACCTTGTTGACTCGGGAATTCGTGAGAGGCTTCGG 420

DB 803 ACCCTGAGAGAGAGTGTGGACCTTGTTGACTCGGGAATTCGTGAGAGGCTTCGG 862
QY 421 AGAACCGGAGAGCTCTGTGCGCCCGCTACATGAACCTGAGCTACGAGACTTGCCTCT 480
DB 863 AGAACCGGAGAGCTCTGTGCGCCCGCTACATGAACCTGAGCTACGAGACTTGCCTCT 922
QY 481 CCATGTTTGAAGAGGCTCATATGATATATCTCCAACTGTGTAACTCTTACGCCACT 540
DB 923 CCATGTTTGAAGAGGCTCATATGATATATCTCCAACTGTGTAACTCTTACGCCACT 982
QY 541 CTGTGAGACAGCTTCTAGTTAGAGCGTCTGTGAATAGTGTGAGAGGAGAACTGTG 600
DB 983 CTGTGAGACAGCTTCTAGTTAGAGCGTCTGTGAATAGTGTGAGAGGAGAACTGTG 1042
QY 601 ACAATTGAGACAGAAACCGGATTCGTGTGAGAAACCAATGAAATGAACTCAGTGT 660
DB 1043 ACAATTGAGACAGAAACCGGATTCGTGTGAGAAACCAATGAAATGAACTCAGTGT 1102
QY 661 AAGAGCTTCTAAAAAGATTTGTGCAAGAAAGAAACTGTTCTTGCATTTCTGAATGT 720
DB 1103 AAGAGCTTCTAAAAAGATTTGTGCAAGAAAGAAACTGTTCTTGCATTTCTGAATGT 1162
QY 721 CTTCGCAACAGGAAACAAATGACTTGTCCAAAGTTTAAACAGGCTGATTCAGAA 780
DB 1163 CTTCGCAACAGGAAACAAATGACTTGTCCAAAGTTTAAACAGGCTGATTCAGAA 1222
QY 781 ACCAATGACAGATTTGAGATTTATCACAGTTGATGTCTCAAGTGAAGAGCAACT 840
DB 1223 ACCAATGACAGATTTGAGATTTATCACAGTTGATGTCTCAAGTGAAGAGCAACT 1282
QY 841 CTTTCAACCAAGTTTCAAGCAATTCGAGAGAGGTTGTGGGCAATGAGATTAATCTCA 900
DB 1283 CTTTCAACCAAGTTTCAAGCAATTCGAGAGAGGTTGTGGGCAATGAGATTAATCTCA 1342
QY 901 TGAAGATCATCTTTGGAGATTTCTGTAGTTTGAATCAGACAAAGTTTGCAGAA 960
DB 1343 TGAAGATCATCTTTGGAGATTTCTGTAGTTTGAATCAGACAAAGTTTGCAGAA 1402
QY 961 GGAAGTGTGAGTGTGATGAGAAAGTCTTGGACATTAACAGCAATGAGGAGATTTCA 1020
DB 1403 GGAAGTGTGAGTGTGATGAGAAAGTCTTGGACATTAACAGCAATGAGGAGATTTCA 1462
QY 1021 GGCACCATGAGGAGTGTGATGAGAAAGTCTTGGACATTAACAGCAATGAGGAGATTTCA 1080
DB 1463 GGCACCATGAGGAGTGTGATGAGAAAGTCTTGGACATTAACAGCAATGAGGAGATTTCA 1522
QY 1081 GAACTCCAGCTCAGGCTTACCAAAATGAAAGTTGCCAGGCTTGGAGAGGAAAGAT 1140
DB 1523 GAACTCCAGCTCAGGCTTACCAAAATGAAAGTTGCCAGGCTTGGAGAGGAAAGAT 1582
QY 1141 ATCATCATCTGCTCTCTTACAGGAGTGAAGAAACAGAGTGGCTTTTACATTTGCCAAG 1200
DB 1583 ATCATCATCTGCTCTCTTACAGGAGTGAAGAAACAGAGTGGCTTTTACATTTGCCAAG 1642
QY 1201 GATCACTTACAGAGAGAGAGAGAGATGTGAGCTGAGAAAGTTATATCTTGTCAAT 1260
DB 1643 GATCACTTACAGAGAGAGAGAGAGATGTGAGCTGAGAAAGTTATATCTTGTCAAT 1702
QY 1261 AAGGTAAGTGTGATGAGAGAGTCTTCCGAGAGGAGTTTCAACATTTTGAAGAAATGG 1320
DB 1703 AAGGTAAGTGTGATGAGAGAGTCTTCCGAGAGGAGTTTCAACATTTTGAAGAAATGG 1762
QY 1321 TATCGTGTATTTGATTAAGGTATACCAATGAAATATCAATTTTCAGAAAGTTGTC 1380
DB 1763 TATCGTGTATTTGATTAAGGTATACCAATGAAATATCAATTTTCAGAAAGTTGTC 1822
QY 1381 AAGTCTGTGATTAATTAATACAGTACAGTCAAAATCTTTGAAAACTCCCTTTAAACTTG 1440
DB 1823 AAGTCTGTGATTAATTAATACAGTACAGTCAAAATCTTTGAAAACTCCCTTTAAACTTG 1882
QY 1441 GAAATGAGAGAGTGTGTGATTAATTTCTCAATTTTCCCTCATTAATCATTTGATGAA 1500

Db 1883 GAAATGAGAGAGTCTGGTGTTCATTGTCTCACTTTCCCTCATTAATCATGTATGAA 1942
 Qy 1501 TGTTCATCAGACCAACAAGAGAGTGTATTAATTAATCATCAGGACATTATTTGATGAG 1560
 Db 1943 TGTTCATCAGACCAACAAGAGAGTGTATTAATTAATCATCAGGACATTATTTGATGAG 2002
 Qy 1561 AAGTTGAAAAACAATAGACTCAAGAAAAAACAACAGATGATCCCTTCTCTAGATA 1620
 Db 2003 AAGTTGAAAAACAATAGACTCAAGAAAAAACAACAGATGATCCCTTCTCTAGATA 2062
 Qy 1621 CTGGGCTAAAGCTTCACTGGTGTGTGAGGGGGCCACGAGAGAACGCAAGAGTGAAGA 1680
 Db 2063 CTGGGCTAAAGCTTCACTGGTGTGTGAGGGGGCCACGAGAGAACGCAAGAGTGAAGA 2122
 Qy 1681 CACATTTTAAACTATGTGCAATCTTGATGCAATTACTATTAATCTGTTAAAGAAAC 1740
 Db 2123 CACATTTTAAACTATGTGCAATCTTGATGCAATTACTATTAATCTGTTAAAGAAAC 2182
 Qy 1741 CTTGATCAACTGMAAAACCAATATACAGAGCCATGCAAGAGTTTCCATTCAGATGCA 1800
 Db 2183 CTTGATCAACTGMAAAACCAATATACAGAGCCATGCAAGAGTTTCCATTCAGATGCA 2242
 Qy 1801 ACCAGAGAGATCATTTTAAGGAACTTTGAAATATATGCAAGATTCAACTTAT 1860
 Db 2243 ACCAGAGAGATCATTTTAAGGAACTTTGAAATATATGCAAGATTCAACTTAT 2302
 Qy 1861 TGTCAATGATGCAATGTCAGATTTTGAACCTCAACCCATGACAAATGGGCAATTC 1920
 Db 2303 TGTCAATGATGCAATGTCAGATTTTGAACCTCAACCCATGACAAATGGGCAATTC 2362
 Qy 1921 ATGMAAAAAAGCTCAAAAAAGAAATCGCAAGAAAGCTGTTGTGCAAGAACATTTG 1980
 Db 2363 ATGMAAAAAAGCTCAAAAAAGAAATCGCAAGAAAGCTGTTGTGCAAGAACATTTG 2422
 Qy 1981 AGGAGTACATAGAGCCCTCAAAATTAATGACAAATTCGAAATGATGCTATACT 2040
 Db 2423 AGGAGTACATAGAGCCCTCAAAATTAATGACAAATTCGAAATGATGCTATACT 2482
 Qy 2041 CATCTTGAACCTTCTATATATGAAAGAAAGATTAAGATTCGATCAGATGAGATGAT 2100
 Db 2483 CATCTTGAACCTTCTATATATGAAAGAAAGATTAAGATTCGATCAGATGAGATGAT 2542
 Qy 2101 AGTATGAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Db 2543 AGTATGAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2602
 Qy 2161 AAACCTTTGAACTGATGAAACAGATGATTTCTCATGACCTTATTTTGAACCAAT 2220
 Db 2603 AAACCTTTGAACTGATGAAACAGATGATTTCTCATGACCTTATTTTGAACCAAT 2662
 Qy 2221 AAAATGTTGAAAGGCTGCTGAAAAACCAAGATTAAGAAATGAAAGCTGACCAATTA 2280
 Db 2663 AAAATGTTGAAAGGCTGCTGAAAAACCAAGATTAAGAAATGAAAGCTGACCAATTA 2722
 Qy 2281 AGAATATACATATGAGCAATATATAGAGCTGAGAAATCAGACGAGAGATTAATCTTT 2340
 Db 2723 AGAATATACATATGAGCAATATATAGAGCTGAGAAATCAGACGAGAGATTAATCTTT 2782
 Qy 2341 ACAAAAAACGACAGAGTGCATATGCGCTTCCACATGATTAATCTGAAAAATGAAAAATTT 2400
 Db 2783 ACAAAAAACGACAGAGTGCATATGCGCTTCCACATGATTAATCTGAAAAATGAAAAATTT 2842
 Qy 2401 GCTGAAGTATGAGTCAAAAGCCCAATCTGATTTGAGCTGACACAGCAGTGAATCAAA 2460
 Db 2843 GCTGAAGTATGAGTCAAAAGCCCAATCTGATTTGAGCTGACACAGCAGTGAATCAAA 2902
 Qy 2461 CCCATGACACAGATGAAACAAAAGAGATTAATGATTAATGCACTGAAAAATCAAT 2520
 Db 2903 CCCATGACACAGATGAAACAAAAGAGATTAATGATTAATGCACTGAAAAATCAAT 2962
 Qy 2521 CTGCTTATGCTTACCAAGTGGCAGAAAGATCTGAGATTAATGAAGATGTAACATTTGTT 2580
 Db 2963 CTGCTTATGCTTACCAAGTGGCAGAAAGATCTGAGATTAATGAAGATGTAACATTTGTT 3022

Qy 2581 ATCCGTTATGCTCTGTCACCAATGAAATAGCCATGCTCAGGCCGCTGAGCCAGA 2640
 Db 3023 ATCCGTTATGCTCTGTCACCAATGAAATAGCCATGCTCAGGCCGCTGAGCCAGA 3082
 Qy 2641 GCTGATGAGAGCACTTACGCTCTGTTGCTCACAGTGTTCAGAGATTATCCAACTGAG 2700
 Db 3083 GCTGATGAGAGCACTTACGCTCTGTTGCTCACAGTGTTCAGAGATTATCCAACTGAG 3142
 Qy 2701 ACAGTTAATGATTTCCGAGAGAGATGATGTATTAAGCTATTCATTTGTTCAAAATATG 2760
 Db 3143 ACAGTTAATGATTTCCGAGAGAGATGATGTATTAAGCTATTCATTTGTTCAAAATATG 3202
 Qy 2761 AAACGAGAGATGATGCTCATTAAGATTTTGAATTAACATGCAAGATTAATGAAAAA 2820
 Db 3203 AAACGAGAGATGATGCTCATTAAGATTTTGAATTAACATGCAAGATTAATGAAAAA 3262
 Qy 2821 AAATGAAAAACCAAGAAATTTTGCAGAGCTTACAGAAATTAACCATCACTTAATACT 2880
 Db 3263 AAATGAAAAACCAAGAAATTTTGCAGAGCTTACAGAAATTAACCATCACTTAATACT 3322
 Qy 2881 TTCTCTTGAACAACTGACGTGCTAGCTGCTGTTGAGGAAATATCCATGTAATGAG 2940
 Db 3323 TTCTCTTGAACAACTGACGTGCTAGCTGCTGTTGAGGAAATATCCATGTAATGAG 3382
 Qy 2941 AAATGATCATCAGTCAATATGACCCAGAAATCAAGAACTTTTACATTTGAAGAAAAAC 3000
 Db 3383 AAATGATCATCAGTCAATATGACCCAGAAATCAAGAACTTTTACATTTGAAGAAAAAC 3442
 Qy 3001 AAAGCATGCAAAAGAGTGTGCTCCGACTATCAAAATTAATGTAATCATCTGCAATGT 3060
 Db 3443 AAAGCATGCAAAAGAGTGTGCTCCGACTATCAAAATTAATGTAATCATCTGCAATGT 3502
 Qy 3061 GGCAGAGCTTGGGGAACATATGATGTCGCAAAAGCTTATGTTGCTGCTCAAAATA 3120
 Db 3503 GGCAGAGCTTGGGGAACATATGATGTCGCAAAAGCTTATGTTGCTGCTCAAAATA 3562
 Qy 3121 AGGAATTTTGTAGTGTGTTTCAAAAAATTAATCAACAAAGAAATCAAAAGTGGGTA 3180
 Db 3563 AGGAATTTTGTAGTGTGTTTCAAAAAATTAATCAACAAAGAAATCAAAAGTGGGTA 3622
 Qy 3181 GAATTAACCTATCAATTTCCCAATCTTGAATTCATGAAATGCTGTTATTTAGTATGAG 3240
 Db 3623 GAATTAACCTATCAATTTCCCAATCTTGAATTCATGAAATGCTGTTATTTAGTATGAG 3682
 Qy 3241 GATAGCACTTGTATGAAATCTTTTAATAATCAATCAATGTTAACTTAATATGATTA 3300
 Db 3683 GATAGCACTTGTATGAAATCTTTTAATAATCAATCAATGTTAACTTAATATGATTA 3742
 Qy 3301 TGATTAATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
 Db 3743 TGATTAATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3802
 Qy 3361 CTCTG 3365
 Db 3803 CTCTG 3807

RESULT 9
 ADN04879
 ID ADN04879 standard; cDNA, 3379 BP.
 XX
 AC ADN04879;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Antiprosclerotic cDNA sequence #654.
 XX
 KW ds; gene; antiprosclerotic; gene therapy; psoriasis; diagnosis.
 OS Homo sapiens.
 PN WO2004028479-A2.

XX 08-APR-2004.
PD 25-SEP-2003; 2003WO-US030907.
PF 25-SEP-2002; 2002US-0414006P.
PR (GETH) GENENTECH INC.
PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu JD;
XX WPI, 2004-305105/28.
DR P-PSDB; ADN04880.
XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 1; SEQ ID NO 1273; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC creating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX
SQ Sequence 3379 BP; 1152 A; 644 C; 753 G; 830 T; 0 U; 0 Other;
Query Match 99.6%; Score 3353; DB 12; Length 3379;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3364; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCGCGCGGCGCTAGAGACCCTGTGACAAACCTGTCATTGTGAGGACAGAGCGGTAGAC 60
DB 1 GCGCGCGGCGCTAGAGACCCTGTGACAAACCTGTCATTGTGAGGACAGAGCGGTAGAC 60
QY 61 CCGCTCTTCTTAAGTGGGCGAGCGGACGCGGACGACATTTTCACTGTCGCGACAGAA 120
DB 61 CCGCTCTTCTTAAGTGGGCGAGCGGACGCGGACGACATTTTCACTGTCGCGACAGAA 120
QY 121 CAGACACATCTGCTTGGGAGAAACCTCTCCCTTCTCTGAGAAAGAAAGTGTGAATGGG 180
DB 121 CAGACACATCTGCTTGGGAGAAACCTCTCCCTTCTCTGAGAAAGAAAGTGTGAATGGG 180
QY 181 TATTCCACAGACGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCAGGCGTGAATG 240
DB 181 TATTCCACAGACGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCAGGCGTGAATG 240
QY 241 TACATCCAGGTGAGGCGCTGTGCTGACTACCTGACCTTTTCTGCTGCAAGGTGAAGAG 300
DB 241 TACATCCAGGTGAGGCGCTGTGCTGACTACCTGACCTTTTCTGCTGCAAGGTGAAGAG 300
QY 301 CAGATTCAGAGGACGATCGCCACCTCCGAGGACATGACGAGCAATTGAATGCTGTGAGC 360
DB 301 CAGATTCAGAGGACGATCGCCACCTCCGAGGACATGAGGCAATTGAATGCTGTGAGC 360
QY 361 ACCTTGAAGAGGAGCTGTGAGCCTTGTGAGCTCGGGAATTCGAGAGGCGCTCCG 420
DB 361 ACCTTGAAGAGGAGCTGTGAGCCTTGTGAGCTCGGGAATTCGAGAGGCGCTCCG 420
QY 421 AGAAGCGGACGCCCTGTGCGCGCCGCTATACATGAACCTTGAAGTCAAGGACTTGCCT 480
DB 421 AGAAGCGGACGCCCTGTGCGCGCCGCTATACATGAACCTTGAAGTCAAGGACTTGCCT 480
QY 481 CCATCGTTTGAAGACGCTCATGATGAATATCTCCAACTGTGAACCTCTTCCAGCCACT 540
DB 481 CCATCGTTTGAAGACGCTCATGATGAATATCTCCAACTGTGAACCTCTTCCAGCCACT 540
QY 541 CTGGTGAACAAGCTTCTAGTTAGAGAGCTTGTGAGATTAAGGACATGAGAGGAACTGTTG 600
DB 541 CTGGTGAACAAGCTTCTAGTTAGAGAGCTTGTGAGATTAAGGACATGAGAGGAACTGTTG 600

QY 601 ACAATTGAAGACAGAAACCGGATTTGCTGTCAGAGAAACAATGGAATGAATCAGGTGTA 660
DB 601 ACAATTGAAGACAGAAACCGGATTTGCTGTCAGAGAAACAATGGAATGAATCAGGTGTA 660
QY 661 AGAGAGCTACTAAAAAGATTTGTGCAAGAAAGAAAATGCTGCTCATTTCTGTAATGTT 720
DB 661 AGAGAGCTACTAAAAAGATTTGTGCAAGAAAGAAAATGCTGCTCATTTCTGTAATGTT 720
QY 721 CTTTCGTAACAGAGAAACAATGAACCTTGTCCAGAGTTTAAAGGCTCTGATTTGCTCAGAA 780
DB 721 CTTTCGTAACAGAGAAACAATGAACCTTGTCCAGAGTTTAAAGGCTCTGATTTGCTCAGAA 780
QY 781 AGCAATGACAGATTTGAGAAATTTATCAAGTTGATGCTCAAGTGAAGAGCAACT 840
DB 781 AGCAATGACAGATTTGAGAAATTTATCAAGTTGATGCTCAAGTGAAGAGCAACT 840
QY 841 CTTTCACACAGATTTCAGCCAAATCTGAGAGAGAGTCTGGGAGATGAGAAATTAATCTCA 900
DB 841 CTTTCACACAGATTTCAGCCAAATCTGAGAGAGAGTCTGGGAGATGAGAAATTAATCTCA 900
QY 901 TCAGAAATCATCTTTTGCAGATTTCTTGTGATTTCAAGATCAACACAAAGTTTGCAGAA 960
DB 901 TCAGAAATCATCTTTTGCAGATTTCTTGTGATTTCAAGATCAACACAAAGTTTGCAGAA 960
QY 961 GGAAGTGTACGCTGCTTGAATGAATGAAGTCTGGAATCAATACAGCAATGAGGAGTATCA 1020
DB 961 GGAAGTGTACGCTGCTTGAATGAATGAAGTCTGGAATCAATACAGCAATGAGGAGTATCA 1020
QY 1021 GGCACCATGGAAGTGAATTCAGATGAAGAGATGTGCGACAAAGACATCCCGGAGCCA 1080
DB 1021 GGCACCATGGAAGTGAATTCAGATGAAGAGATGTGCGACAAAGACATCCCGGAGCCA 1080
QY 1081 GAATTCACAGCTCAGGCTTTACCAAAATGGAAGTTGCCAGCCAGCTTGAAGAGGAAGAT 1140
DB 1081 GAATTCACAGCTCAGGCTTTACCAAAATGGAAGTTGCCAGCCAGCTTGAAGAGGAAGAT 1140
QY 1141 ATCATCATCTGCTCTCCCTACAGGAGTGAAGAAACAAGTGGCTGTTTACATTCGCCAAG 1200
DB 1141 ATCATCATCTGCTCTCCCTACAGGAGTGAAGAAACAAGTGGCTGTTTACATTCGCCAAG 1200
QY 1201 GATCACTTGAAGAGAAAGAAAGATCTGAGCTTGAAAGATTAAGTTCTTGTCAAT 1260
DB 1201 GATCACTTGAAGAGAAAGAAAGATCTGAGCTTGAAAGATTAAGTTCTTGTCAAT 1260
QY 1261 AAGGTATGCTGATTTGAAGACAGCTCTTCCGCAAGAGTTCCAACATTTTGAAGAAATG 1320
DB 1261 AAGGTATGCTGATTTGAAGACAGCTCTTCCGCAAGAGTTCCAACATTTTGAAGAAATG 1320
QY 1321 TATCGGTATTTGATTAAGTGTGATACCCAACTGAAATATCAATTTCCAGAAAGTTGTC 1380
DB 1321 TATCGGTATTTGATTAAGTGTGATACCCAACTGAAATATCAATTTCCAGAAAGTTGTC 1380
QY 1381 AAGTCTGTGATTAATTAATTCAGTACAGTCAAACTCTTGAAGAACTCCCTTTAAACTTG 1440
DB 1381 AAGTCTGTGATTAATTAATTCAGTACAGTCAAACTCTTGAAGAACTCCCTTTAAACTTG 1440
QY 1441 GAAATGAGAGAGATGCTGTTCAATTTGTCAGACTTTTCCCTCATTAATCAATGATGA 1500
DB 1441 GAAATGAGAGAGATGCTGTTCAATTTGTCAGACTTTTCCCTCATTAATCAATGATGA 1500
QY 1501 TGTCTATCACACCAACAAAGAACAGTGTATTAACATTAAGAGCATTAATTTGATGAG 1560
DB 1501 TGTCTATCACACCAAC-AAGAACAGTGTATTAACATTAAGAGCATTAATTTGATGAG 1560
QY 1561 AAGTTGAAGAAACAATGACTCAAGAAAGAAACAAACAGATATTCCTCTCTCAGATA 1620
DB 1561 AAGTTGAAGAAACAATGACTCAAGAAAGAAACAAACAGATATTCCTCTCTCAGATA 1620
QY 1621 CTGGGACTAACAGCTTCACTGTGTGTGAGAGGGCCACGAGCAAGCCAAAGCTGAAGAA 1680
DB 1621 CTGGGACTAACAGCTTCACTGTGTGTGAGAGGGCCACGAGCAAGCCAAAGCTGAAGAA 1680
QY 1681 CACATTTTAAACATATGTGCCAATCTTGTATGCAATTAATTAACCTGTAAAGAAAAC 1740


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Db      ||||| 1680 CACATTTTAAACCTATGTCCTATGTCATTTTAACTGTTTAAAGAAAAC 1739
Qy      ||||| 1741 CTGTGATCACTGAAAAACCAATATACAGAGCCATGACAGAGTTGGCATTCAGATGCA 1800
Db      ||||| 1740 CTGTGATCACTGAAAAACCAATATACAGAGCCATGACAGAGTTGGCATTCAGATGCA 1799
Qy      ||||| 1801 ACCAGAGAGATCATTTTAAAGAAACCTTCTAGAAATATAGCAAGATTCAAACTTAT 1860
Db      ||||| 1800 ACCAGAGAGATCATTTTAAAGAAACCTTCTAGAAATATAGCAAGATTCAAACTTAT 1859
Qy      ||||| 1861 TGTCAATGATGTCATGTCATGATTTTGGAACTCAACCTATGAAACATGAGCCATTCA 1920
Db      ||||| 1860 TGTCAATGATGTCATGTCATGATTTTGGAACTCAACCTATGAAACATGAGCCATTCA 1919
Qy      ||||| 1921 ATGGAAAAAAGCTGCAAAAAAAGAAATGCGAAAGAAAGCTGTTGTGACAGAACTTTG 1980
Db      ||||| 1920 ATGGAAAAAAGCTGCAAAAAAAGAAATGCGAAAGAAAGCTGTTGTGACAGAACTTTG 1979
Qy      ||||| 1981 AGGAAGTACATGAGGCTCTACAAATTTATGACACAAATTCGATGATGATGCTATGCT 2040
Db      ||||| 1980 AGGAAGTACATGAGGCTCTACAAATTTATGACACAAATTCGATGATGATGCTATGCT 2039
Qy      ||||| 2041 CATCTTGAACCTTTCTATATATGAGAGAAAGATTAAGAGTTTGCACTCATAGAGATGAT 2100
Db      ||||| 2040 CATCTTGAACCTTTCTATATATGAGAGAAAGATTAAGAGTTTGCACTCATAGAGATGAT 2099
Qy      ||||| 2101 AGTGAATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Db      ||||| 2100 AGTGAATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2159
Qy      ||||| 2161 AAACCTTTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Db      ||||| 2160 AAACCTTTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2219
Qy      ||||| 2221 AAAATGTTGAAAAGGCTGCTGAAAAACCAAGATATGAAATGAAAAGCTGACCAATTA 2280
Db      ||||| 2220 AAAATGTTGAAAAGGCTGCTGAAAAACCAAGATATGAAATGAAAAGCTGACCAATTA 2279
Qy      ||||| 2281 AGAATATCATATATGAGACATATATATAGAGCTGAGAGATTCAGACAGAGAAATATCTTT 2340
Db      ||||| 2280 AGAATATCATATATGAGACATATATATAGAGCTGAGAGATTCAGACAGAGAAATATCTTT 2339
Qy      ||||| 2341 ACAAACACGACAGAGTGCATATGCGCTTCCAGTGAATTAAGTGAATGAAAATTT 2400
Db      ||||| 2340 ACAAACACGACAGAGTGCATATGCGCTTCCAGTGAATTAAGTGAATGAAAATTT 2399
Qy      ||||| 2401 GCTGAAGTGAAGTCAAAAGCCCAACATCTGATTTGAGCTGACACAGCAGTGAATCAAA 2460
Db      ||||| 2400 GCTGAAGTGAAGTCAAAAGCCCAACATCTGATTTGAGCTGACACAGCAGTGAATCAAA 2459
Qy      ||||| 2461 CCCATGACACAGAAATGAAACAAAAGAAAGTCAATAGTAAATTTGCGCTGAAAAATCAAT 2520
Db      ||||| 2460 CCCATGACACAGAAATGAAACAAAAGAAAGTCAATAGTAAATTTGCGCTGAAAAATCAAT 2519
Qy      ||||| 2521 CTGCTTATGCTACACAGTGCAGAGAAAGGCTGAGATTAATTAAGATTAATCAATGTT 2580
Db      ||||| 2520 CTGCTTATGCTACACAGTGCAGAGAAAGGCTGAGATTAATTAAGATTAATCAATGTT 2579
Qy      ||||| 2581 ATCCGTTATGCTCTGCTACCAATGAAATAGCCATGATCCAGGCCGCTGCTGAGCCAGA 2640
Db      ||||| 2580 ATCCGTTATGCTCTGCTACCAATGAAATAGCCATGATCCAGGCCGCTGCTGAGCCAGA 2639
Qy      ||||| 2641 GCTGATGAGAGCACTGACGTCCTGCTGCTCACAAGTGTTCAGAGATTAATGCAATGAG 2700
Db      ||||| 2640 GCTGATGAGAGCACTGACGTCCTGCTGCTCACAAGTGTTCAGAGATTAATGCAATGAG 2699
Qy      ||||| 2701 ACAGTTAATGATTTCCAGAGAAAGATGATTAAGCTATTAATCATGTTCAAAATGAG 2760
Db      ||||| 2700 ACAGTTAATGATTTCCAGAGAAAGATGATTAAGCTATTAATCATGTTCAAAATGAG 2759
Qy      ||||| 2761 AAACGAGAGATGCTCATAGATTTTGAATTAAGATGCAAGTCAAAAGTAAATGAAAAG 2820

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Db      ||||| 2760 AAACGAGAGATGCTCATATAGATTTTGAATTAAGATGCAAGTCAAAAGTAAATGAAAAG 2819
Qy      ||||| 2821 AAATGAAAACCAAGAGAAATATATGCAAGATTAACAAAGATTAACCAATCACTAAATCT 2880
Db      ||||| 2820 AAATGAAAACCAAGAGAAATATATGCAAGATTAACAAAGATTAACCAATCACTAAATCT 2879
Qy      ||||| 2881 TTCTTTGCAAAAACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db      ||||| 2880 TTCTTTGCAAAAACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2939
Qy      ||||| 2941 AAATGCAATCACTGCAATTAATGACCCCAATTAATGCAAGAACTTATGATGTAAGAGAAAAC 3000
Db      ||||| 2940 AAATGCAATCACTGCAATTAATGACCCCAATTAATGCAAGAACTTATGATGTAAGAGAAAAC 2999
Qy      ||||| 3001 AAAGCATGCAAAAAGAGTGTGCGCATCTATCAATTAATGGAATATCATGCAAAATGT 3060
Db      ||||| 3000 AAAGCATGCAAAAAGAGTGTGCGCATCTATCAATTAATGGAATATCATGCAAAATGT 3059
Qy      ||||| 3061 GGCAGGCTTGGGGAACAATGATGTCACAAAGCTTATGATTTGCTGCTCAAAATA 3120
Db      ||||| 3060 GGCAGGCTTGGGGAACAATGATGTCACAAAGCTTATGATTTGCTGCTCAAAATA 3119
Qy      ||||| 3121 AGGAATTTTGTATGCTTTTCAAAATTAATTAACAAAGAAACATTAACAAAGTGGGTA 3180
Db      ||||| 3120 AGGAATTTTGTATGCTTTTCAAAATTAATTAACAAAGAAACATTAACAAAGTGGGTA 3179
Qy      ||||| 3181 GAATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGATGAT 3240
Db      ||||| 3180 GAATTAACCTATCAATTTCCCAATCTTGAATGATGATGATGATGATGATGATGATGATGAT 3239
Qy      ||||| 3241 GATTGACCTTGAATGAAAGATTTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3300
Db      ||||| 3240 GATTGACCTTGAATGAAAGATTTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3299
Qy      ||||| 3301 TGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3360
Db      ||||| 3300 TGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3359
Qy      ||||| 3361 CTCTG 3365
Db      ||||| 3360 CTCTG 3364

RESULT 10
AD022237
ID AD022237 standard; DNA; 3668 BP.
XX
AC AD022237;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5057.
XX
KW soft tissue sarcoma; cyrostatic; gene therapy; vaccine; screening; human;
XX
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003MO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlocnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression

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PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX
PS Example 2; SEQ ID NO 5057; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX
SQ Sequence 3668 BP; 1215 A; 730 C; 811 G; 872 T; 0 U; 40 Other;

Query Match 99.2%; Score 3339.2; DB 12; Length 3668;

Best Local Similarity 99.3%; Pred. No. 0; Mismatches 24; Indels 0; Gaps 0;

Matches 3341; Conservative 0;

1 GCGCGCGCGCTGAGAGCCCTGTGACAACTGCTGATTGTGAGCAGAGCGGTAGAC 60

1 GCGCGCGCGCTGAGAGCCCTGTGACAACTGCTGATTGTGAGCAGAGCGGTAGAC 60

61 CCTGCTTCTTAAGTGGGAGCGGAGCGGAGCGGAGCAATTTCACTGTCGCGAGACAA 120

61 CCTGCTTCTTAAGTGGGAGCGGAGCGGAGCGGAGCAATTTCACTGTCGCGAGACAA 120

61 CCTGCTTCTTAAGTGGGAGCGGAGCGGAGCGGAGCAATTTCACTGTCGCGAGACAA 120

121 CAGCAGCACTGCTTGGGAGAAACCTCTCCCTCTCTGAGAAAGAAATGCGATGAG 180

121 CAGCAGCACTGCTTGGGAGAAACCTCTCCCTCTCTGAGAAAGAAATGCGATGAG 180

121 CAGCAGCACTGCTTGGGAGAAACCTCTCCCTCTCTGAGAAAGAAATGCGATGAG 180

181 TATTCACAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 240

181 TATTCACAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 240

181 TATTCACAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 240

241 TACATTCAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 300

241 TACATTCAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 300

241 TACATTCAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 300

301 CAGATTCAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 360

301 CAGATTCAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 360

301 CAGATTCAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 360

361 ACCTTGGAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 420

361 ACCTTGGAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 420

361 ACCTTGGAGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 420

421 AGAAGCGGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 480

421 AGAAGCGGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 480

421 AGAAGCGGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 480

481 CCAATCTTTGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 540

481 CCAATCTTTGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 540

481 CCAATCTTTGAGAGAGATTTCCGCTATCTCATCTCGTCTTCAAGGCGCGGTGAATG 540

QY 721 CTTGCTCAAAACAGAAACATGAACTTGTCCAAAGTTTACAGGCTCTGATTGCTCAGAA 780

QY 721 CTTGCTCAAAACAGAAACATGAACTTGTCCAAAGTTTACAGGCTCTGATTGCTCAGAA 780

QY 721 CTTGCTCAAAACAGAAACATGAACTTGTCCAAAGTTTACAGGCTCTGATTGCTCAGAA 780

QY 781 ACCAATGAGAGATTTGAGATTTTATCAGAGTGTGAGTCCCAAGTGGAGAGCAACT 840

QY 781 ACCAATGAGAGATTTGAGATTTTATCAGAGTGTGAGTCCCAAGTGGAGAGCAACT 840

QY 781 ACCAATGAGAGATTTGAGATTTTATCAGAGTGTGAGTCCCAAGTGGAGAGCAACT 840

QY 841 CTTTCAACACAGTTCAGCAAAATCTGAGAGAGAGTCTGGGAGATGAGAAATTAATCA 900

QY 841 CTTTCAACACAGTTCAGCAAAATCTGAGAGAGAGTCTGGGAGATGAGAAATTAATCA 900

QY 841 CTTTCAACACAGTTCAGCAAAATCTGAGAGAGAGTCTGGGAGATGAGAAATTAATCA 900

QY 901 TGAAGATCATCTTTTGCAGATTTCTTGTGATTTTCAAGATCAGACAAAGTTTGCAGAA 960

QY 901 TGAAGATCATCTTTTGCAGATTTCTTGTGATTTTCAAGATCAGACAAAGTTTGCAGAA 960

QY 901 TGAAGATCATCTTTTGCAGATTTCTTGTGATTTTCAAGATCAGACAAAGTTTGCAGAA 960

QY 961 GGAAGTGCAGTGTCTTGAATGAATGAGTCTGAGATTAACAGCAATGAGGAGATTTCA 1020

QY 961 GGAAGTGCAGTGTCTTGAATGAATGAGTCTGAGATTAACAGCAATGAGGAGATTTCA 1020

QY 961 GGAAGTGCAGTGTCTTGAATGAATGAGTCTGAGATTAACAGCAATGAGGAGATTTCA 1020

QY 1021 GGCACCATGAGAGATTTGAGATTTGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAG 1080

QY 1021 GGCACCATGAGAGATTTGAGATTTGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAG 1080

QY 1021 GGCACCATGAGAGATTTGAGATTTGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAG 1080

QY 1081 GAACTTCAGAGCTGAGGCTTTACCAAAATGAAAGTTGCCAGCCAGCTTGGAGAGAAAT 1140

QY 1081 GAACTTCAGAGCTGAGGCTTTACCAAAATGAAAGTTGCCAGCCAGCTTGGAGAGAAAT 1140

QY 1081 GAACTTCAGAGCTGAGGCTTTACCAAAATGAAAGTTGCCAGCCAGCTTGGAGAGAAAT 1140

QY 1144 ATCATCATCTGCTCCCTTACAGAGAGAGTGAAGAAACAGAGAGAGTGTATTAATGCCAAG 1200

QY 1144 ATCATCATCTGCTCCCTTACAGAGAGAGTGAAGAAACAGAGAGAGTGTATTAATGCCAAG 1200

QY 1144 ATCATCATCTGCTCCCTTACAGAGAGAGTGAAGAAACAGAGAGAGTGTATTAATGCCAAG 1200

QY 1201 GATCACTTACAG 1260

QY 1201 GATCACTTACAG 1260

QY 1201 GATCACTTACAG 1260

QY 1261 AGGTAAGTGTGAG 1320

QY 1261 AGGTAAGTGTGAG 1320

QY 1261 AGGTAAGTGTGAG 1320

QY 1321 TATCGTGTATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1380

QY 1321 TATCGTGTATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1380

QY 1321 TATCGTGTATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1380

QY 1381 AAGTCTGATATTTATTAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1440

QY 1381 AAGTCTGATATTTATTAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1440

QY 1381 AAGTCTGATATTTATTAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1440

QY 1441 GAAATGAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1500

QY 1441 GAAATGAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1500

QY 1441 GAAATGAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1500

QY 1441 GAAATGAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1500

QY 1441 GAAATGAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1500

QY 1501 TGTCAATCAACCAAG 1560

QY 1501 TGTCAATCAACCAAG 1560

QY 1501 TGTCAATCAACCAAG 1560

QY 1561 AAGTGAAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1620

QY 1561 AAGTGAAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1620

QY 1561 AAGTGAAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1620

QY 1561 AAGTGAAGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1620

QY 1621 CTGGAGCTAACAGCTTCACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

QY 1621 CTGGAGCTAACAGCTTCACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

QY 1621 CTGGAGCTAACAGCTTCACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

QY 1681 CACATTTTAAACCTATGAG 1740

QY 1681 CACATTTTAAACCTATGAG 1740

QY 1681 CACATTTTAAACCTATGAG 1740

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

QY 1741 CTTGATCAACCTAAG 1800

Oy	1801	CCGAGAGAATTCATTAAAGAGAACTTCTAGAAATTAAGACAAGATTCGAACCTAT	1860
Dp	1801	ACCAGAGAGATGCCATTAAAGAGAACTTCTAGAAATTAAGACAAGATTCGAACCTAT	1860
Oy	1861	TGTCAAAATGATGCCAATGTCCAGATTTTGGAATCACAACCTATGACAAATGGGCCATTCAA	1920
Dp	1861	TGTCAAAATGATGCCAATGTCCAGATTTTGGAATCACAACCTATGACAAATGGGCCATTCAA	1920
Oy	1921	ATGCAAAAAAAAAGCTGCMAAAAAAGGAAATGGCAAGAACGTGTTTGTGCGAAACTTTG	1980
Dp	1921	ATGCAAAAAAAAAGCTGCMAAAAAAGGAAATGGCAAGAACGTGTTTGTGCGAAACTTTG	1980
Oy	1991	AGGAAGTACAAATGAGGGCCCTACAAATTATGACACAATTCGAATGATGAGCGGTATCT	2040
Dp	1991	AGGAAGTACAAATGAGGGCCCTACAAATTATGACACAATTCGAATGATGAGCGGTATCT	2040
Oy	2041	CATCTTGAACCTTCTATTAATGAGAGAAAGATAAGAAAGTTTGGCAGTCATGGAAGATGAT	2100
Dp	2041	CATCTTGAACCTTCTATTAATGAGAGAAAGATAAGAAAGTTTGGCAGTCATGGAAGATGAT	2100
Oy	2101	AGTGATGAGGGTGGTGAATGATGATGATATTGTGATGTTGATGAAGATGAGAGATTTAAAG	2160
Dp	2101	AGTGATGAGGGTGGTGAATGATGATGATATTGTGATGTTGATGAAGATGAGAGATTTAAAG	2160
Oy	2161	AAACCTTTGAAACCTGSGATGAAACAGATGATTTCTCATGACCTTATTTTTTGAAGAACAT	2220
Dp	2161	AAACCTTTGAAACCTGSGATGAAACAGATGATTTCTCATGACCTTATTTTTTGAAGAACAT	2220
Oy	2221	AAAAATGTTGAAAAAGCGTGGCTGMAAAACCCAGAAATATGAAATATGAAAGCTGACCAAAATTA	2280
Dp	2221	AAAAATGTTGAAAAAGCGTGGCTGMAAAACCCAGAAATATGAAATATGAAAGCTGACCAAAATTA	2280
Oy	2281	AGAAATATCCATATGAGACCAATATATCTAGACTGAGAAATCAGCACGAGAAATATCTTT	2340
Dp	2281	AGAAATATCCATATGAGACCAATATATCTAGACTGAGAAATCAGCACGAGAAATATCTTT	2340
Oy	2341	ACAAAAACACGACAGAGTGCATATGCGCTTTCCCACTGSGATTTACTGAAAAATGAAAAATTT	2400
Dp	2341	ACAAAAACACGACAGAGTGCATATGCGCTTTCCCACTGSGATTTACTGAAAAATGAAAAATTT	2400
Oy	2401	GCTGAAGTAGGAGTCAAAAGCCCAACATCTGATTTGGAGCTGGACACAGCAGTGAATTCNA	2460
Dp	2401	GCTGAAGTAGGAGTCAAAAGCCCAACATCTGATTTGGAGCTGGACACAGCAGTGAATTCNA	2460
Oy	2461	CCCATGACACAGAAATGAACAAAAAGAACTCATTAATTAATTTCCGACTGAAAAATAAT	2520
Dp	2461	CCCATGACACAGAAATGAACAAAAAGAACTCATTAATTAATTTCCGACTGAAAAATAAT	2520
Oy	2521	CTGCTTATCGCTACCACTGCGCAGAGAGAGTCTGATATTTAAAGATGTACATTTGT	2580
Dp	2521	CTGCTTATCGCTACCACTGCGCAGAGAGAGTCTGATATTTAAAGATGTACATTTGT	2580
Oy	2581	ATCCGTTATGCTCTGTCACCAATGAATAGCATGATCCAGAGCCCGGTGTCGAGCCAGA	2640
Dp	2581	ATCCGTTATGCTCTGTCACCAATGAATAGCATGATCCAGAGCCCGGTGTCGAGCCAGA	2640
Oy	2641	GCTGATGAGACCACTCATGCTCTGTTGCTCAGAGTGGTTACGAGATTAATGAAACGTGAG	2700
Dp	2641	GCTGATGAGACCACTCATGCTCTGTTGCTCAGAGTGGTTACGAGATTAATGAAACGTGAG	2700
Oy	2701	ACAGTTAATGATTTCCGAGAGAGATGATGTATTAAGCTATACATTTGTTCCAATATYG	2760
Dp	2701	ACAGTTAATGATTTCCGAGAGAGATGATGTATTAAGCTATACATTTGTTCCAATATYG	2760
Oy	2761	AAACGAGAGAGTATGCTCATPAAGTTTGGAAATTAAGATGCAAGTAAAGTATATGGAANA	2820
Dp	2761	AAACGAGAGAGTATGCTCATPAAGTTTGGAAATTAAGATGCAAGTAAAGTATATGGAANA	2820
Oy	2821	AAAAATGAAAAACCAAGAGAAATATTTGCCAAGCATTTCAAGAAATATCCCATCTATAACT	2880
Dp	2821	AAAAATGAAAAACCAAGAGAAATATTTGCCAAGCATTTCAAGAAATATCCCATCTATAACT	2880
Oy	2881	TTCTTTGCAAAAACTGCAGATGTGCTAGCTGTCTGCGGAGAAAGATATCCATGTATTTGAG	2940

Db	2881	TTCCCTTTGGAAAAAACTGCACTGTCGTAGCCTGTTCTGGGGAGAGTATCCATGTATATGAG	2940
Qy	2941	AAAATGATCACTGCAATATATGACCCAGAAATTCAGGAACTTTACATTGTGAAGAAAC	3000
Db	2941	AAAATGATCACTGCAATATATGACCCAGAAATTCAGGAACTTTACATTGTGAAGAAAC	3000
Qy	3001	AAAGCACTGCAAAAAGAAAGTGGCCGACTATCAAAATAAATGATGAAATCATCTGCAAAATG	3060
Db	3001	AAAGCACTGCAAAAAGAAAGTGGCCGACTATCAAAATAAATGATGAAATCATCTGCAAAATG	3060
Qy	3061	GGCCAGGCTTGGGGAAACAATGATGTGTGCAAAAAGGCTTAGATTGCTGTCTCAAAATA	3120
Db	3061	GGCCAGGCTTGGGGAAACAATGATGTGTGCAAAAAGGCTTAGATTGCTGTCTCAAAATA	3120
Qy	3121	AGGAATTTTGTAGTGTGTTTCAAAAATATTCACAAAGAAACAATACAAAAGTGGGTA	3180
Db	3121	AGGAATTTTGTAGTGTGTTTCAAAAATATTCACAAAGAAACAATACAAAAGTGGGTA	3180
Qy	3181	GAATTACCTTCACATTTCCCATCTTGACTATTCAGAAAGCTGTATTATAGTAGAG	3240
Db	3181	GAATTACCTTCACATTTCCCATCTTGACTATTCAGAAAGCTGTATTATAGTAGAG	3240
Qy	3241	GATTAGACCTTGATGTAAGATTTCTTTTAAATATCTATCAGTTAAACATTTAATATGATTA	3300
Db	3241	GATTAGACCTTGATGTAAGATTTCTTTTAAATATCTATCAGTTAAACATTTAATATGATTA	3300
Qy	3301	TGATTAAATGATTCATTATGCTACAGAACTGACATTAAGAAATCAATAAATGATTTGTTTA	3360
Db	3301	TGATTAAATGATTCATTATGCTACAGAACTGACATTAAGAAATCAATAAATGATTTGTTTA	3360
Qy	3361	CTCTG 3365	
Db	3361	CTCTG 3365	
RESULT 11			
ABAO4908	ID	ABAO4908 standard; cDNA; 3372 BP.	
XX	AC		
XX	ABA04908;		
XX	05-MAR-2002	(first entry)	
XX	Human RNA helicase RH16 coding sequence.		
XX	Human: RH16; RNA helicase; cytosolic; virucide; anti-HIV;		
XX	immunosuppressive; immunostimulatory; antirheumatic; antiarthritic;		
XX	antiarteriosclerotic; osteopathic; antidiabetic; hepatotropic;		
XX	antiinflammatory; cancer; infection; HIV; hepatitis; genetic disease;		
XX	autoimmune disease; graft rejection; vaccine; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	CDS	155..3232	
XX	FT	/*tag= a	
XX	FT	/product= "Human RH16"	
XX	PN	WO200185955-A1.	
XX	PD	15-NOV-2001.	
XX	PF	11-MAY-2001; 2001WO-FR001441.	
XX	PR	11-MAY-2000; 2000FR-00006030.	
XX	PA	(ISTA-) ISTAC.	
XX	PI	(INSP) INST PASTEUR LILIE.	
XX	DR	Bahr G, Cocude C, Capron A;	
XX	WPI; 2002-082898/11.		

DR P-PSDB; AAM47798.
XX New polypeptide, useful for treating and diagnosing cancer or
PT inflammation, and drug screening, comprises a human polynucleotide
PT homologous to RNA helicase.
XX
PS Claim 7, Page 85-89; 114pp; French.
XX
CC The present sequence is the coding sequence for human RH16. RH16 is a
CC 116kDa protein and has homology to RNA helicases (DEXH box). RH16 and
CC its coding sequence are useful for treating cancer; acute or chronic
CC infections (especially by HIV or hepatitis B or C); inherited genetic
CC diseases; (auto) immune diseases (particularly rheumatism, arthritis,
CC arteriosclerosis, osteoporosis and diabetes, but many others listed) and
CC to prevent graft rejection. RH16 and its coding sequence are also useful
CC for inducing, or increasing, the immune response to a vaccine
XX
SQ Sequence 3372 BP; 1157 A; 637 C; 748 G; 830 T; 0 U; 0 Other;
Query Match 99.2%; Score 3338.8; DB 6; Length 3372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3343; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 15 GAGCCCTGTGACACCTGTGATTTGACGACACAGGGGTAGACCTGCTTCTTAG 74
Db 1 GGGCCCTGTGACACCTGTGATTTGACGACACAGGGGTAGACCTGCTTCTTAG 60
QY 75 TGGGACGCGGACGCGGACGACATTTGACCTGCTCCGACAGCAACAGACCATCTGCT 134
Db 61 TGGGACGCGGACGCGGACGACATTTGACCTGCTCCGACAGCAACAGACCATCTGCT 120
QY 135 TGGGAGAACCTCTCTCTCTCTGAGAAAGAAAGATGGAATGGTATTTCACAGACGA 194
Db 121 TGGGAGAACCTCTCTCTCTCTGAGAAAGAAAGATGGAATGGTATTTCACAGACGA 180
QY 195 GAATTTCCGCTATCTATCTGCTGCTTCAAGGGCCAGGGTGAATATGTAATCCAGTGA 254
Db 181 GAATTTCCGCTATCTATCTGCTGCTTCAAGGGCCAGGGTGAATATGTAATCCAGTGA 240
QY 255 GCCTGCTGGAATCTGACCTGCTTCTGCTGACAGGTGAAGAGGACAGATTCAGAGAC 314
Db 241 GCCTGCTGGAATCTGACCTGCTTCTGCTGACAGGTGAAGAGGACAGATTCAGAGAC 300
QY 315 AGTCGCCACCTCCGGGACATGACGAGCAGTTGAATCTGCTGAGCACCCTTGGAGAGG 374
Db 301 AGTCGCCACCTCCGGGACATGACGAGCAGTTGAATCTGCTGAGCACCCTTGGAGAGG 360
QY 375 AGTCGCGACCTTTGTTGGAATCTGCGGAAATTTCTGAGGCCCTCCGAGAACCGGACGCC 434
Db 361 AGTCGCGACCTTTGTTGGAATCTGCGGAAATTTCTGAGGCCCTCCGAGAACCGGACGCC 420
QY 435 TCTGGGCGCGCGCTACATGAACCTGAGCTCACGAGCTTGCCCTCCATCGTTGAGAA 494
Db 421 TCTGGGCGCGCGCTACATGAACCTGAGCTCACGAGCTTGCCCTCCATCGTTGAGAA 480
QY 495 CGCTCATGATGATATCTCAATGCTGTAACCTCTTCAAGCCCACTCTGCTGAGCAAGCT 554
Db 481 CGCTCATGATGATATCTCAATGCTGTAACCTCTTCAAGCCCACTCTGCTGAGCAAGCT 540
QY 555 TCTAGTTAAGAGCTTTGGATTAAGTCATGAGAGGAACTGTTGAATTAAGAAACAG 614
Db 541 TCTAGTTAAGAGCTTTGGATTAAGTCATGAGAGGAACTGTTGAATTAAGAAACAG 600
QY 615 AAACCGGATGCTGCTGAGAAACAAATGAAATGATCAGGTGAAGAGCTACTAA 674
Db 601 AAACCGGATGCTGCTGAGAAACAAATGAAATGATCAGGTGAAGAGCTACTAA 660
QY 675 AAGGATTTGACAGAAAGAAACTGTTCTCTGCAATTTGCAATGTTCTTCTCAACAG 734
Db 661 AAGGATTTGACAGAAAGAAACTGTTCTCTGCAATTTGCAATGTTCTTCTCAACAG 720
QY 735 AAACAATGAATTTGCTCAAGAGTTAAACAGGCTTGAATGCTCAAGAAAGCATGACAGAT 794
Db 721 AAACAATGAATTTGCTCAAGAGTTAAACAGGCTTGAATGCTCAAGAAAGCATGACAGAT 780

QY 795 TGAGAAATTTATCACAAGTTGATGATCTTCAAGTGAAGAGCACTTTTCAACACAGT 854
Db 781 TGAGAAATTTATCACAAGTTGATGATCTTCAAGTGAAGAGCACTTTTCAACACAGT 840
QY 855 TGAGCAATCTTGAGAAAGAGGCTGGGGCATGAGAAATATCTATCAATCTCTTT 914
Db 841 TGAGCAATCTTGAGAAAGAGGCTGGGGCATGAGAAATATCTATCAATCTCTTT 900
QY 915 TGCAGATCTTCTGATGTTTGAATCAAGACACAGATTTGGAGAGAGAGTGCAGCTG 974
Db 901 TGCAGATCTTCTGATGTTTGAATCAAGACACAGATTTGGAGAGAGAGTGCAGCTG 960
QY 975 CTGATGAAAGCTTTGACATTAACAGCAATGCGGCAAGTATTCAGGACCATGAGAG 1034
Db 961 CTGATGAAAGCTTTGACATTAACAGCAATGCGGCAAGTATTCAGGACCATGAGAG 1020
QY 1035 TGATTCAGATGAAAGATGTTGGCAGCAAGAGCATCCCGGAGCCAGAACTGACGTCAG 1094
Db 1021 TGATTCAGATGAAAGATGTTGGCAGCAAGAGCATCCCGGAGCCAGAACTGACGTCAG 1080
QY 1095 GCCTTACCAATGAAAGTTGCCAGCCAGCTTGGAGGAGAAATATCATCATCTGCT 1154
Db 1081 GCCTTACCAATGAAAGTTGCCAGCCAGCTTGGAGGAGAAATATCATCATCTGCT 1140
QY 1155 CCTTACAGGAGTGAAGAAACCAAGATGGCTTTTACATTCGCAAGATCACTTACACA 1214
Db 1141 CCTTACAGGAGTGAAGAAACCAAGATGGCTTTTACATTCGCAAGATCACTTACACA 1200
QY 1215 GAAAGAAAGAGATCTGAGCCCTGGAAGATTAATTTCTGTCATTAAGATCTGCTGT 1274
Db 1201 GAAAGAAAGAGATCTGAGCCCTGGAAGATTAATTTCTGTCATTAAGATCTGCTGT 1260
QY 1275 TGAACAGCTCTTCCGCAAGAGTTCACCAATTTTGAAGAAATGATTCGTTATTGG 1334
Db 1261 TGAACAGCTCTTCCGCAAGAGTTCACCAATTTTGAAGAAATGATTCGTTATTGG 1320
QY 1335 ATTAAGTGTGATTAACCAATCTGAAATATCATTTTCAGAAATGTCATGCTGTGAT 1394
Db 1321 ATTAAGTGTGATTAACCAATCTGAAATATCATTTTCAGAAATGTCATGCTGTGAT 1380
QY 1395 TATTTACGATCACTCAATCTTGAAGATCTCCCTTTTAACTTGAAGAAATGAGAGAA 1454
Db 1381 TATTTACGATCACTCAATCTTGAAGATCTCCCTTTTAACTTGAAGAAATGAGAGAA 1440
QY 1455 TGTGTGTTCAATTTGTGACATTTTCCCTCATTAATGATGATGATCATCACCA 1514
Db 1441 TGTGTGTTCAATTTGTGACATTTTCCCTCATTAATGATGATGATCATCACCA 1500
QY 1515 CAAAGAGCAGTGTATTAATTAATCATGATGAGCATTATTTGATCAGAAATGAAAAA 1574
Db 1501 CAAAGAGCAGTGTATTAATTAATCATGATGAGCATTATTTGATCAGAAATGAAAAA 1560
QY 1575 TTAGCTCAAGAAAGAAACAAACAGATGATTTCCCTTCTCAGATTAAGTGAACAG 1634
Db 1561 TTAGCTCAAGAAAGAAACAAACAGATGATTTCCCTTCTCAGATTAAGTGAACAG 1620
QY 1635 TTCACTGTTGTTGAGGGGCGCAGAGCAAGCAAGAGCTGAAGAACATTTTAAACT 1694
Db 1621 TTCACTGTTGTTGAGGGGCGCAGAGCAAGCAAGAGCTGAAGAACATTTTAAACT 1680
QY 1695 ATGTGCAATCTTGAATGATTTTAACTTTAACTTTAAAGAAACCTTGATCACTGA 1754
Db 1681 ATGTGCAATCTTGAATGATTTTAACTTTAACTTTAAAGAAACCTTGATCACTGA 1740
QY 1755 AAACCAATATCAGAGCCATGCAAGAGTTTCCATTCAGATGCAACCAAGAGATTC 1814
Db 1741 AAACCAATATCAGAGCCATGCAAGAGTTTCCATTCAGATGCAACCAAGAGATTC 1800
QY 1815 ATTTAAAGGAACCTTCTAGAAATTAATGACAGATTTCAACTTATTTGCAATGATTC 1874
Db 1801 ATTTAAAGGAACCTTCTAGAAATTAATGACAGATTTCAACTTATTTGCAATGATTC 1860

XX The invention relates to 971 novel human cDNA sequences (ADCC29919-
CC ADCC30889) and the polypeptides they encode (ADCC30890-ADCC31660). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADCC1861-ADCC32627) and the polypeptides encoded by the contigs (ADCC32628
CC -ADCC3394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.
XX

Sequence 3446 BP; 1184 A; 649 C; 772 G; 841 T; 0 U; 0 Other;

Query Match 98.5%; Score 3316.2; DB 10; Length 3446;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3321; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 36 CATTTCAGGACAGAGCGGTAGACCTGCTCTTAAGTGGGACGGACAGCGGACAG 95
DB 104 CACTTCAGGACAGAGCGGTAGACCTGCTCTTAAGTGGGACGGACAGCGGACAG 163
QY 96 CACATTTCACCTGTCCCGGACAGACACACATCTGCTTGGAGAACCTCTCCCTTC 155
DB 164 CACATTTCACCTGTCCCGGACAGACACACATCTGCTTGGAGAACCTCTCCCTTC 223
QY 156 CTGAGAAAGAAAGATGTCGATGGTATTCACAGACGAGAAATTCCTGCTATCTC 215
DB 224 CTGAGAAAGAAAGATGTCGATGGTATTCACAGACGAGAAATTCCTGCTATCTC 283
QY 216 GTGCTTCAGGACAGAGGTGAAATGTAATCCAGGTGGAGCCGTGCTGACATCACTGC 275
DB 284 GTGCTTCAGGACAGAGGTGAAATGTAATCCAGGTGGAGCCGTGCTGACATCACTGC 343
QY 276 CTTTTCGCTGAGAGGTGAGAGAGATTTCAGAGACAGTGGCACTCCGGAAACAT 335
DB 344 CTTTTCGCTGAGAGGTGAGAGAGATTTCAGAGACAGTGGCACTCCGGAAACAT 403
QY 336 GCAGGAGATTGAATCTGCTGAGACCTTGGAGAAAGAGTGTGGCACTTGGTTGAC 395
DB 404 GCAGGAGATTGAATCTGCTGAGACCTTGGAGAAAGAGTGTGGCACTTGGTTGAC 463
QY 396 TGGGGAATTCGTGAGAGCCCTCCGGAGAACCGGACACCTCTGGCCCGCGTACATGAA 455
DB 464 TGGGGAATTCGTGAGAGCCCTCCGGAGAACCGGACACCTCTGGCCCGCGTACATGAA 523
QY 456 CCCTGAGCTCAGGAGCTTGCCTCTCCATGCTTTGAGAACGCTCATGATGATATCTCCA 515
DB 524 CCCTGAGCTCAGGAGCTTGCCTCTCCATGCTTTGAGAACGCTCATGATGATATCTCCA 583
QY 516 ACTGCTGAACCTTCCTGAGCCACTCTGTGAGCAAGCTTCTAGTTAGAGACGTCTTGA 575

DB 584 ACTGCTGAACCTTCCTGAGCCACTCTGTGAGCAAGCTTCTAGTTAGAGACGTCTTGA 643
QY 576 TAAAGTCATGAGAGAGAACTGTTGACATTTGAGACAGAAACCGGATTTGCTGTCAGA 635
DB 644 TAAAGTCATGAGAGAGAACTGTTGACATTTGAGACAGAAACCGGATTTGCTGTCAGA 703
QY 636 AAACAATGAATGAATCAGGTGTAGAGAGCTACTTAAAGAAATTTGTCAGAAAGAAA 695
DB 704 AAACAATGAATGAATCAGGTGTAGAGAGCTACTTAAAGAAATTTGTCAGAAAGAAA 763
QY 696 CTGCTTCCTGCAATTTGCAATGTTCTTGTCMAACAGAAACATGAACTTGTCCAGA 755
DB 764 CTGCTTCCTGCAATTTGCAATGTTCTTGTCMAACAGAAACATGAACTTGTCCAGA 823
QY 756 GTTAAACAGCTCTGATTTGTCAGAAAGACATGACAGATTGAGAAATTTATCAAGTTGA 815
DB 824 GTTAAACAGCTCTGATTTGTCAGAAAGACATGACAGATTGAGAAATTTATCAAGTTGA 883
QY 816 TGGTCTCCTCAAGTGAAGAGCAACTTCTTCAACCAAGTTACGCCAATCTGAGAGAGA 875
DB 884 TGGTCTCCTCAAGTGAAGAGCAACTTCTTCAACCAAGTTACGCCAATCTGAGAGAGA 943
QY 876 GGTCTGGGACATGAGAAATTAATCTCATGAATCATCTTTGACAGATTCTGTAGTTTC 935
DB 944 GGTCTGGGACATGAGAAATTAATCTCATGAATCATCTTTGACAGATTCTGTAGTTTC 1003
QY 936 AGAATCAGACACAAGTTTGGCAGAAAGAAAGTGTCACTGCTTGAATGAAAGTCTTGACA 995
DB 1004 ABAATCAGACACAAGTTTGGCAGAAAGAAAGTGTCACTGCTTGAATGAAAGTCTTGACA 1063
QY 996 TAAACGCAACATGGGACATGATTCAGGACCACTGGGAAAGTATTCAGATGAAAGAAAT 1055
DB 1064 TAAACGCAACATGGGACATGATTCAGGACCACTGGGAAAGTATTCAGATGAAAGAAAT 1123
QY 1056 GGACAGAAAGACATCCCGGACAGAACTCCAGCTCAGGCTTACCAATGGAAGTTGC 1115
DB 1124 GGACAGAAAGACATCCCGGACAGAACTCCAGCTCAGGCTTACCAATGGAAGTTGC 1183
QY 1116 CCAGCAGCTTGAAGAGAAAGAAATATCATCATCTGCTCCCTACAGGAGGTGAAAAAC 1175
DB 1184 CCAGCAGCTTGAAGAGAAAGAAATATCATCATCTGCTCCCTACAGGAGGTGAAAAAC 1243
QY 1176 CAGAGTGTGTTTACATTTGCCAGAGATCATTTAGACAAAGAAAAAGCATCTGAGCC 1235
DB 1244 CAGAGTGTGTTTACATTTGCCAGAGATCATTTAGACAAAGAAAAAGCATCTGAGCC 1303
QY 1236 TGAAGAAAGTAAAGTCTTGTCAATTAAGGTACTGCTAGTTGAACAGCTTCGCGAAGA 1295
DB 1304 TGAAGAAAGTAAAGTCTTGTCAATTAAGGTACTGCTAGTTGAACAGCTTCGCGAAGA 1363
QY 1296 GTTCAACCATTTTGAAGAAATGATCTGTTATTTGATTTAAGTGTGATACCAACT 1355
DB 1364 GTTCAACCATTTTGAAGAAATGATCTGTTATTTGATTTAAGTGTGATACCAACT 1423
QY 1356 GAAATATATCTTCAAGAAAGTTGCAAGTCTGTGATATTTATCACTCACTCAAT 1415
DB 1424 GAAATATATCTTCAAGAAAGTTGCAAGTCTGTGATATTTATCACTCACTCAAT 1483
QY 1416 CTTTGAAGAACTCCCTTAAATTTGAGAAATGGAAGATGCTGTGTTCAATTTGTCGA 1475
DB 1484 CTTTGAAGAACTCCCTTAAATTTGAGAAATGGAAGATGCTGTGTTCAATTTGTCGA 1543
QY 1476 CTTTTCCTCATTTATCATTTGATGATGATCATCAACCAAGAAAGAGCTATATATA 1535
DB 1544 CTTTTCCTCATTTATCATTTGATGATGATCATCAACCAAGAAAGAGCTATATATA 1603
QY 1536 CATCATAGAGCATTTATTTGATGACAGAGTTGAAAAACAATAGACTCAAGAAAGAAACA 1595
DB 1604 CATCATAGAGCATTTATTTGATGACAGAGTTGAAAAACAATAGACTCAAGAAAGAAACA 1663
QY 1596 ACCAGATATTCCTCTCCATGATCTGAGAACTTACAGCTTCACTGGGTGAGAGGAC 1655

Db 1664 ACCAGTATCCCTCTCAGATACCTGGGACTTAACAGCTTCACTGGTGTGGAGGGCC 1723
 Qy 1656 CACGAGCAAGCCAAAGCTGAAGACACATTTTAAACTATGTGCCAATCTTGATGCAT 1715
 Db 1724 CACGAGCAAGCCAAAGCTGAAGACACATTTTAAACTATGTGCCAATCTTGATGCAT 1783
 Qy 1716 TACTATTAACCTGTTAAAGAAAACCTTGATCACTGAATAAACCAATACAGAGCCATG 1775
 Db 1784 TACTATTAACCTGTTAAAGAAAACCTTGATCACTGAATAAACCAATACAGAGCCATG 1843
 Qy 1776 CAGAGAGTTGGCATTTGCAATGCAACAGAGAGATCCATTTAAAGAAAACCTTGATCA 1835
 Db 1844 CAGAGAGTTGGCATTTGCAATGCAACAGAGAGATCCATTTAAAGAAAACCTTGATCA 1903
 Qy 1836 AATTAATGACAGAGATTCAAACTTATGTCAATGAGTCCATGTCAGATTTTGGAACTCA 1895
 Db 1904 AATTAATGACAGAGATTCAAACTTATGTCAATGAGTCCATGTCAGATTTTGGAACTCA 1963
 Qy 1896 ACCCTATGAAACAATGGGCCATTCAAATGAAAAAAAAGCTGCAAAAAAGAAATCGCAA 1955
 Db 1964 ACCCTATGAAACAATGGGCCATTCAAATGAAAAAAAAGCTGCAAAAAAGAAATCGCAA 2023
 Qy 1956 AGAAGGTGTTTGGCAGAACATTTGAGAGATCAATGAGCCCTTCAAAATTAATGACAC 2015
 Db 2024 AGAAGGTGTTTGGCAGAACATTTGAGAGATCAATGAGCCCTTCAAAATTAATGACAC 2083
 Qy 2016 AATTCGAATGATAGATGCGTATCTCATCTTGAAAACCTTCTAATATGAGAGAAAGATA 2075
 Db 2084 AATTCGAATGATAGATGCGTATCTCATCTTGAAAACCTTCTAATATGAGAGAAAGATA 2143
 Qy 2076 GAAGTTTGCAGTCATAGAAAGATGATAGTGAAGGGTGTGATGATGATGATTTGTGATG 2135
 Db 2144 GAAGTTTGCAGTCATAGAAAGATGATAGTGAAGGGTGTGATGATGATGATTTGTGATG 2203
 Qy 2136 TGATGAAGATGAGATGATTTAAAGAAACCTTTGAACTGATGAAACGATGATTTCT 2195
 Db 2204 TGATGAAGATGAGATGATTTAAAGAAACCTTTGAACTGATGAAACGATGATTTCT 2263
 Qy 2196 CATGACTTATTTTGAAGAAACAATAAAGTGTGAAGAGCTGGCTGAAGAACCCAGATA 2255
 Db 2264 CATGACTTATTTTGAAGAAACAATAAAGTGTGAAGAGCTGGCTGAAGAACCCAGATA 2323
 Qy 2256 TGAATAATGAAAAGCTGACCAAAATTAAGAAATACCATATGAGCATATATAGACTGA 2315
 Db 2324 TGAATAATGAAAAGCTGACCAAAATTAAGAAATACCATATGAGCATATATAGACTGA 2383
 Qy 2316 GGAATCAGACAGAGAAATATCTTTACAAAAACAGACAGAGTGCATATGCCCTTCCCA 2375
 Db 2384 GGAATCAGACAGAGAAATATCTTTACAAAAACAGACAGAGTGCATATGCCCTTCCCA 2443
 Qy 2376 GTGGAATTAATGAAAATGAAAATTTGCTGAAGAGATCAAAAGCCACATCTGATTTGG 2435
 Db 2444 GTGGAATTAATGAAAATGAAAATTTGCTGAAGAGATCAAAAGCCACATCTGATTTGG 2503
 Qy 2436 ACCTGACACAGACAGTGTCAAAACCATGACACAGATGAAACAAAAGAAAGTCAATAG 2495
 Db 2504 ACCTGACACAGACAGTGTCAAAACCATGACACAGATGAAACAAAAGAAAGTCAATAG 2563
 Qy 2496 TAAATTTGCTGACTGAAAAATCAATCTGTTATCGCTTACACAGTGGCAGAAAGAGTCT 2555
 Db 2564 TAAATTTGCTGACTGAAAAATCAATCTGTTATCGCTTACACAGTGGCAGAAAGAGTCT 2623
 Qy 2556 GGAATTAATGAAATGTAACATTTGTTATCGGTATGCTCTGCTGACCAATGAAATAGCCAT 2615
 Db 2624 GGAATTAATGAAATGTAACATTTGTTATCGGTATGCTCTGCTGACCAATGAAATAGCCAT 2683
 Qy 2616 GGTCCAGGCCCGTGTGAGCCAGAGCTGATGAGACACTGATGCTGTTGCTCAGAG 2675
 Db 2684 GGTCCAGGCCCGTGTGAGCCAGAGCTGATGAGACACTGATGCTGTTGCTCAGAG 2743
 Qy 2676 TGGTTCAAGAGTTATCGAAATGAGACAGTTAATGATTTCCAGAGAGATGATGTATA 2735
 Db 2744 TGGTTCAAGAGTTATCGAAATGAGACAGTTAATGATTTCCAGAGAGATGATGTATA 2803

Qy 2736 AGCTATACATTTGTGTTCAAAATATGAAACACAGAGAGATATGCTCATTAAGATTTGGAATT 2795
 Db 2804 AGCTATACATTTGTGTTCAAAATATGAAACACAGAGAGATATGCTCATTAAGATTTGGAATT 2863
 Qy 2796 ACAGATGCAAGATATATGAAAAAGAAAATGAAAACCAAGAGAAATATTTGCCAACATTA 2855
 Db 2864 ACAGATGCAAGATATATGAAAAAGAAAATGAAAACCAAGAGAAATATTTGCCAACATTA 2923
 Qy 2856 CAAGATTAACCATCACTATATATCTTCTGCAAAAATGTCAGTGTGCTAGCCGTTC 2915
 Db 2924 CAAGATTAACCATCACTATATATCTTCTGCAAAAATGTCAGTGTGCTAGCCGTTC 2983
 Qy 2916 TGGGGAAGATATCATGTTATTTAGAAAAATGATCATGATCATATATGACCCAGAAATGCA 2975
 Db 2984 TGGGGAAGATATCATGTTATTTAGAAAAATGATCATGATCATATATGACCCAGAAATGCA 3043
 Qy 2976 GGAATCTTACATTTGTAAGAAAAACAAGACATGCAAAAGAGTGTGCCACTATCAAT 3035
 Db 3044 GGAATCTTACATTTGTAAGAAAAACAAGACATGCAAAAGAGTGTGCCACTATCAAT 3103
 Qy 3036 AAATGTAATCATCTGCAAAATGAGCAGCTTGAGGGAACAATGATGTGCACAAAG 3095
 Db 3104 AAATGTAATCATCTGCAAAATGAGCAGCTTGAGGGAACAATGATGTGCACAAAG 3163
 Qy 3096 CTTAGATTTGCTGCTCAAAATAGAAATTTGTAGTGTGTTCAAAATATATTCAC 3155
 Db 3164 CTTAGATTTGCTGCTGCTCAAAATAGAAATTTGTAGTGTGTTCAAAATATATTCAC 3223
 Qy 3156 AAAGAAACATACAAAAAGTGGTGAATTAATCAATTCATCACTTTCCCAATCTTGACTATTC 3215
 Db 3224 AAAGAAACATACAAAAAGTGGTGAATTAATCAATTCATCACTTTCCCAATCTTGACTATTC 3283
 Qy 3216 AGAATGCTTTATTTAGATGAGATTTAGACCTGATGAAATGCTTTTAAATACT 3275
 Db 3284 AGAATGCTTTATTTAGATGAGATTTAGACCTGATGAAATGCTTTTAAATACT 3343
 Qy 3276 ATCAGTTAAACATTTAATATGATTTATGATTAATGATTTCAATATGCTACAGAACTGACAT 3335
 Db 3344 ATCAGTTAAACATTTAATATGATTTATGATTAATGATTTCAATATGCTACAGAACTGACAT 3403
 Qy 3336 AAGAAATCAATTAATGATTTGTTTACTCT 3364
 Db 3404 AAGAAATCAATTAATGATTTGTTTACTCT 3432

RESULT 13
 AAD11170
 ID AAD11170 strand; DNA; 3131 BP.
 AC AAD11170;
 XX
 DT 29-NOV-2001 (first entry)
 XX
 DE Human melanoma differentiation associated-5 protein-related DNA.
 XX
 KW Human melanoma differentiation associated gene; Mda-5; interferon; IFN;
 KW RNA helicase motif; caspase recruitment domain; CARD; therapy; melanoma;
 KW neuroblastoma; astrocytoma; glioblastoma; multifactor; cancer; cervical;
 KW breast; colon; prostate; osteosarcoma; chromosarcoma; systemic toxicity;
 KW central nervous system; cytosolic; apoptosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200164707-A1.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006960.
 XX
 PR 29-FEB-2000; 2000US-00515363.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.

XX Fisher PB, Kang D, GopalKrishnan RV;
PI
XX WPI; 2001-565494/63.
XX
XX Nucleic acid sequences encoding a Melanoma Differentiation Associated
PT Gene useful for cancer cell growth suppression, apoptosis and anti-viral
PT activity.
PS Disclosure; Page 134-148; 152pp; English.
XX
XX The present invention relates to an isolated nucleic acid encoding a
CC melanoma differentiation associated gene-5 (mda-5) polypeptide. Mda-5
CC contains a caspase recruitment domain (CARD) and a RNA helicase motif.
CC Mda-5 is a novel interferon (IFN) inducible gene with structural
CC similarities to RNA helicases and CARD motif containing proteins. Mda-5
CC is induced during terminal differentiation in human melanoma cells
CC treated with the combination of recombinant fibroblast IFN and the
CC anti-leukemic compound mezerein (MEZ). Mda-5 is useful for identifying
CC compounds that may induce its expression. Mda-5 is useful for treating
CC cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma
CC multiforme, cervical cancer, breast cancer, colon cancer, prostate
CC cancer, osteosarcoma, chondrosarcoma and especially where the cancer is a
CC cancer of the central nervous system and apoptosis. The mda-5 promoter
CC exhibits melanocyte tissue specificity and minimises systemic toxicity.
CC The present sequence is human Mda-5 protein-related DNA. Note: The
CC present sequence is designated SEQ ID NO:2 in the sequence listing, but
CC does not correspond to the sequence designated SEQ ID NO:2 in the main
CC body of the specification (AAE10155). The present sequence is not further
CC referred to in the specification, and has been represented in a protein
CC format in the sequence listing
XX
SQ Sequence 3131 BP; 1075 A; 583 C; 699 G; 774 T; 0 U; 0 Other;
Query Match 92.2%; Score 3104; DB 4; Length 3131;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3129; Conservative 0; Mismatches 0; Indels 5; Gaps 2;
QY 169 ATGTGAAATGGGTATTCACAGACGAAATTCGCTATCTCATCTCGTTCAGAGCC 228
DB 1 ATGTGAAATGGGTATTCACAGACGAAATTCGCTATCTCATCTCGTTCAGAGCC 60
QY 229 AGGGTAAATGTACATCCAGGTGAGCCTGTGCTGACTACTGACCTTTCTGCTGCA 288
DB 61 AGGGTAAATGTACATCCAGGTGAGCCTGTGCTGACTACTGACCTTTCTGCTGCA 120
QY 289 GAGGTGAAGAGAGATTCAGAGACAGTCGACCTCCGGGAAATGAGGAGGTGAA 348
DB 121 GAGGTGAAGAGAGATTCAGAGACAGTCGACCTCCGGGAAATGAGGAGGTGAA 180
QY 349 CTGCTGCTGAGCACTTGGAGAGAGGTCTGGCACTTGTGTGACTCGGGAATTCGTG 408
DB 181 CTGCTGCTGAGCACTTGGAGAGAGGTCTGGCACTTGTGTGACTCGGGAATTCGTG 240
QY 409 GAGGCTTCGGAGAAACCGGACGCTTGGCCGCCGCTACATGAACTTGAAGTCAAG 468
DB 241 GAGGCTTCGGAGAAACCGGACGCTTGGCCGCCGCTACATGAACTTGAAGTCAAG 300
QY 469 GACTTGCCCTCCACGCTTGGAGAGCGTCATGATGATATCTCCACCTGCGAAACCTC 528
DB 301 GACTTGCCCTCCACGCTTGGAGAGCGTCATGATGATATCTCCACCTGCGAAACCTC 360
QY 529 CTTTACGCCACTCTGTGAGCAAGCTTCTAGTTAGAGAGCTGTGATAGTCAAGAG 588
DB 361 CTTTACGCCACTCTGTGAGCAAGCTTCTAGTTAGAGAGCTGTGATAGTCAAGAG 420
QY 589 GAGGAACCTGTGACAAATTGAAGACAGAAACCGGATTCCTGTCAGAGAAACAATGAAAT 648
DB 421 GAGGAACCTGTGACAAATTGAAGACAGAAACCGGATTCCTGTCAGAGAAACAATGAAAT 480
QY 649 GAATCAGGTGTAGAGAGCTACTAAAGAGATTGTGACAGAAAGAAACTGTGTTCTTGA 708
DB 481 GAATCAGGTGTAGAGAGCTACTAAAGAGATTGTGACAGAAAGAAACTGTGTTCTTGA 540

QY 709 TTTCTGAATGTTCTTGTGCAACAGAGAAACAATGAACCTTGTCCAGAGTTAAAGGCTCT 768
DB 541 TTTCTGAATGTTCTTGTGCAACAGAGAAACAATGAACCTTGTCCAGAGTTAAAGGCTCT 600
QY 769 GATTGCTAGAAAGCAATGACAGATGAGATTTATACAAATGATGATGCTCTCAATG 828
DB 601 GATTGCTAGAAAGCAATGACAGATGAGATTTATACAAATGATGATGCTCTCAATG 660
QY 829 GAAAGCAACTTCTTCAACCAACAGTTCAGCCAAATCTGAGAGAGAGGCTTGGGCAATG 888
DB 661 GAAAGCAACTTCTTCAACCAACAGTTCAGCCAAATCTGAGAGAGAGGCTTGGGCAATG 720
QY 889 GAGATTAATCTATCAGAAATCATCTTTTGCAGATTTCTTGTAGTTTCAGATTCAGACA 948
DB 721 GAGATTAATCTATCAGAAATCATCTTTTGCAGATTTCTTGTAGTTTCAGATTCAGACA 780
QY 949 AGTTGGCAGAAAGAGAGTGCAGCTGCTTGAATGAAAGTCTTGACATPAACAGCAATG 1008
DB 781 AGTTGGCAGAAAGAGAGTGCAGCTGCTTGAATGAAAGTCTTGACATPAACAGCAATG 840
QY 1009 GGCAGTGAATTCAGGACCATGGAGATGATTCAGATGAAGAGATGCGACAGCAAGCA 1068
DB 841 GGCAGTGAATTCAGGACCATGGAGATGATTCAGATGAAGAGATGCGACAGCAAGCA 900
QY 1069 TCCCGGAGCCAGAACTCAGCTCAGGCTTACCAATGGAAGTTGCCAGCAGCTTGG 1128
DB 901 TCCCGGAGCCAGAACTCAGCTCAGGCTTACCAATGGAAGTTGCCAGCAGCTTGG 960
QY 1129 GAAAGGAAGATATCATCATCTGCTCCCTCAGGAGATGGAAAAACAGAGTGCCTGT 1188
DB 961 GAAAGGAAGATATCATCATCTGCTCCCTCAGGAGATGGAAAAACAGAGTGCCTGT 1020
QY 1189 TACATTGGCCAGAGATCACTTACACAAAGAAAGAAAAAGCATGTGACCTGAAATATATA 1248
DB 1021 TACATTGGCCAGAGATCACTTACACAAAGAAAGAAAAAGCATGTGACCTGAAATATATA 1080
QY 1249 GTTCTTGTCAATAGGTACTGTAGTGAACAGCTCTTCCGAGAGATTTCCAAACATTT 1308
DB 1081 GTTCTTGTCAATAGGTACTGTAGTGAACAGCTCTTCCGAGAGATTTCCAAACATTT 1140
QY 1309 TTGAAGAAATGGTATCGTTATTGATTAAGTGTGATACCAACTGAAATATCATTT 1368
DB 1141 TTGAAGAAATGGTATCGTTATTGATTAAGTGTGATACCAACTGAAATATCATTT 1200
QY 1369 CCAGAAAGTGTCAAGTCTGTGATATTAATACATGACGCTCAATCTTGAATACTCC 1428
DB 1201 CCAGAAAGTGTCAAGTCTGTGATATTAATACATGACGCTCAATCTTGAATACTCC 1257
QY 1429 CTCTTAAACTTGAAGATGAGAGAGATGCTGTTCATTTGTCAAGCTTTTCCCTCATTT 1488
DB 1258 CTCTTAAACTTGAAGATGAGAGAGATGCTGTTCATTTGTCAAGCTTTTCCCTCATTT 1317
QY 1489 ATCATTTGATGATATGATCAACCAACCAAGAGAGATTAATATCATCATGAGGAT 1548
DB 1318 ATCATTTGATGATATGATCAACCAACCAAGAGAGATTAATATCATCATGAGGAT 1377
QY 1549 TATTGATGACAGAAATTTGAAAAACAATAGACTCAAGAAAGAAAAACAACAGATTTCC 1608
DB 1378 TATTGATGACAGAAATTTGAAAAACAATAGACTCAAGAAAGAAAAACAACAGATTTCC 1437
QY 1609 CTTCTCAGATATCTGGACATAACAGCTTCACTGCTGTGAGAGGCGCACAGACAGCC 1668
DB 1438 CTTCTCAGATATCTGGACATAACAGCTTCACTGCTGTGAGAGGCGCACAGACAGCC 1497
QY 1669 AAAGCTGAAGAACATTTTAAACTATAGTGCATCTTATGATCTTTATTAATTAACCT 1728
DB 1498 AAAGCTGAAGAACATTTTAAACTATAGTGCATCTTATGATCTTTATTAATTAACCT 1557
QY 1729 GTTAAAGAAAACCTTGATCACTGAAAAACCAATATACAGAGCCATGCAAGAAAGTTTGC 1788
DB 1558 GTTAAAGAAAACCTTGATCACTGAAAAACCAATATACAGAGCCATGCAAGAAAGTTTGC 1617

QY 1789 ATTGCAGATGCAACGAGAGAGATCCATTAAAGAGAACTCTTAGAATATGACAAAG 1848
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 Db 1618 ATTGCAGATGCAACGAGAGAGATCCATTAAAGAGAACTCTTAGAATATGACAAAG 1677
 |||||
 QY 1849 ATTCAAACTTATGTGAAATGATCCAGTCTGATTTTGAACCTCAACCTTGAACAA 1908
 |||||
 Db 1678 ATTCAAACTTATGTGAAATGATCCAGTCTGATTTTGAACCTCAACCTTGAACAA 1737
 |||||
 QY 1909 TGGGCATTTCAAATGCAAAAAAGCTGCAAAAAAGAAATGCAAAAGACCTGTTTG 1968
 |||||
 Db 1738 TGGGCATTTCAAATGCAAAAAAGCTGCAAAAAAGAAATGCAAAAGACCTGTTTG 1797
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 QY 1969 GCAGAACATTGAGAGAGTCAATGAGGCTTCAAAATTATGACAAATTTGAATGATA 2028
 |||||
 Db 1798 GCAGAACATTGAGAGAGTCAATGAGGCTTCAAAATTATGACAAATTTGAATGATA 1857
 |||||
 QY 2029 GAT - GCGTATCTCATCTTGGAACTTTCTATATGAGAGAAAGATTAAGATTTGCG 2086
 |||||
 Db 1858 GATCCGCGTATCTCATCTTGGAACTTTCTATATGAGAGAAAGATTAAGATTTGCG 1917
 |||||
 QY 2087 TCATAGAGATGATGATGATGAGGCTGATGATGATGATGATGATGATGATGATGATG 2146
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 Db 1918 TCATAGAGATGATGATGATGAGGCTGATGATGATGATGATGATGATGATGATGATG 1977
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 QY 2147 AGGATGATTTAAAGAAACCTTTGAACTGATGAAACAGATGATTTCTCATGACTTTAT 2206
 |||||
 Db 1978 AGGATGATTTAAAGAAACCTTTGAACTGATGAAACAGATGATTTCTCATGACTTTAT 2037
 |||||
 QY 2207 TTTTGAAGAAACATTAATGTTGAAAGGCTGCTGAAACCCAGAAATGAAATGAA 2266
 |||||
 Db 2038 TTTTGAAGAAACATTAATGTTGAAAGGCTGCTGAAACCCAGAAATGAAATGAA 2097
 |||||
 QY 2267 AGGTGCAAAATTAAGAAATACATATGAGCAATATCTAGACTGAGGATTCAGCAC 2326
 |||||
 Db 2098 AGGTGCAAAATTAAGAAATACATATGAGCAATATCTAGACTGAGGATTCAGCAC 2157
 |||||
 QY 2327 GAGGATTAATCTTTACAAAAACGACAGAGTGCATATGCGCTTCCAGTGGATTAAG 2386
 |||||
 Db 2158 GAGGATTAATCTTTACAAAAACGACAGAGTGCATATGCGCTTCCAGTGGATTAAG 2217
 |||||
 QY 2387 AAAATGAAAAATTTGCTGAAGTGAAGTCAAGCCCATCTGATTTGAGCTGACAC 2446
 |||||
 Db 2218 AAAATGAAAAATTTGCTGAAGTGAAGTCAAGCCCATCTGATTTGAGCTGACAC 2277
 |||||
 QY 2447 GCAGTGAAGTCAAGCCCATGACAGAGTGAAGTCAAGAAAGGATTTAGAAATTTGCG 2506
 |||||
 Db 2278 GCAGTGAAGTCAAGCCCATGACAGAGTGAAGTCAAGAAAGGATTTAGAAATTTGCG 2337
 |||||
 QY 2507 CTGGAATAATCAATCTGCTTATGCTACCAAGTGCAGAAAGGCTTGGATTTAAAG 2566
 |||||
 Db 2338 CTGGAATAATCAATCTGCTTATGCTACCAAGTGCAGAAAGGCTTGGATTTAAAG 2397
 |||||
 QY 2567 AATGTAACATTTGTTATCCGTTATGCTGCTACCAATGAATAGCCATGCTCAGGCC 2626
 |||||
 Db 2398 AATGTAACATTTGTTATCCGTTATGCTGCTACCAATGAATAGCCATGCTCAGGCC 2457
 |||||
 QY 2627 GTGCTGAGGCAAGCTGATGAGACCTTAAGTCTGCTGCTCAAGTGTTCAGAG 2686
 |||||
 Db 2458 GTGCTGAGGCAAGCTGATGAGACCTTAAGTCTGCTGCTCAAGTGTTCAGAG 2517
 |||||
 QY 2687 TTATGACATGAGACGTTATGATTTCCGAGAGAAAGATGATGATTAAGCTATACAT 2746
 |||||
 Db 2518 TTATGACATGAGACGTTATGATTTCCGAGAGAAAGATGATGATTAAGCTATACAT 2577
 |||||
 QY 2747 GTGTTCAAAATATGAACAGAGAGATGCTCATAGATTTTGAATTTACAGATCAAA 2806
 |||||
 Db 2578 GTGTTCAAAATATGAACAGAGAGATGCTCATAGATTTTGAATTTACAGATCAAA 2637
 |||||
 QY 2807 GTTATATGAAAAAATGAAAAACAGAGAAATTTGCGAAGCATTTACAGAAATPACC 2866
 |||||
 Db 2638 GTTATATGAAAAAATGAAAAACAGAGAAATTTGCGAAGCATTTACAGAAATPACC 2697
 |||||
 QY 2867 CATCACTAATACTTCTTGGAAAAACGAGTGTGCTGCTGTTGCGGGAAGATA 2926

Db 2698 CATCACTAATACTTCTTGGAAAAACGAGTGTGCTGCTGTTGCGGGAAGATA 2757
 |||||
 QY 2927 TCCATGTAATTTGAAAAATGATCAAGTCAATATGACCCAGAAATTAAGAACTTTACA 2986
 |||||
 Db 2758 TCCATGTAATTTGAAAAATGATCAAGTCAATATGACCCAGAAATTAAGAACTTTACA 2817
 |||||
 QY 2987 TTGTAAGAAAAACAAAGCATGCAAAAGAGTGTGCGCACTATCAAAATTAAGTGA 3046
 |||||
 Db 2818 TTGTAAGAAAAACAAAGCATGCAAAAGAGTGTGCGCACTATCAAAATTAAGTGA 2877
 |||||
 QY 3047 TCATCTGCAAAATGTGCGCAGGCTTGGGGAACATGATGTGCAAAAGCTTGAATTC 3106
 |||||
 Db 2878 TCATCTGCAAAATGTGCGCAGGCTTGGGGAACATGATGTGCAAAAGCTTGAATTC 2937
 |||||
 QY 3107 CTGTGCTCAAAATTAAGAAATTTGTAGTGTGTTTCAAAATTAATCAAAAGAAACAT 3166
 |||||
 Db 2938 CTGTGCTCAAAATTAAGAAATTTGTAGTGTGTTTCAAAATTAATCAAAAGAAACAT 2997
 |||||
 QY 3167 ACAAAAAGTGGTAGAATTAATCACTATCAATTTCCAAATCTTGAATTCAGAAATGCTGT 3226
 |||||
 Db 2998 ACAAAAAGTGGTAGAATTAATCACTATCAATTTCCAAATCTTGAATTCAGAAATGCTGT 3057
 |||||
 QY 3227 TATTAGTATGAGATTAAGCACTTGATTAAGATTTCTTTAAATTAATCACTTAAC 3286
 |||||
 Db 3058 TATTAGTATGAGATTAAGCACTTGATTAAGATTTCTTTAAATTAATCACTTAAC 3117
 |||||
 QY 3287 ATTTAATATGATTA 3300
 |||||
 Db 3118 ATTTAATATGATTA 3131
 |||||
 RESULT 14
 ADJ75813
 ID ADJ75813 standard; DNA; 3771 BP.
 XX
 AC ADJ75813;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene SBO ID NO:1065.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 XX
 KM respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 XX
 OS gene therapy; marker gene; gene; ds.
 XX
 OS Mus musculus.
 XX
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 XX
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX
 DR WPI; 2004-19315/19.
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 XX
 PT comparing the expression level of a marker gene in a biological sample
 XX
 PT from a subject with the expression level of the gene in a sample from a
 XX
 PT healthy subject.
 XX
 PS Claim 14; SBO ID NO 1065; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 XX
 CC or chronic obstructive pulmonary disease. The method comprises
 XX
 CC determining the expression level of a marker gene in a biological sample

CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (1) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.

SO Sequence 3771 BP; 1183 A; 821 C; 866 G; 901 T; 0 U; 0 Other;

Query Match 65.5%; Score 2202.4; DB 12; Length 3771;

Best Local Similarity 80.7%; Pred. No. 0; Mismatches 616; Indels 7; Gaps 3;

Matches 2609; Conservative 0;

121 CAGCACCATCTGCTGGAGAACCTCTCCCTCTCTCTGAGAAAGAAATGCGATG 179
186 CCGCCCGCCCGCCCGGAGACTCTCTCCATTTCTGAGACCTCAACATGCGATG 245
180 GATATTCACAGAGAGAAATTTCCGCTATCTCATCTGCTGAGGCGCAAGGTAAT 239
246 CTGTTCTGAGAGAGAGAGCTTCAAGATCTCATCTTATCTTCAGGCCAGGCTGAAAT 305
240 GTCATCTCAGTGGAGACCTGCTGATCTACCTGACCTTTGCTGAGAGAGTAAAG 299
306 GTCATCTCAGTGGAGACCTGCTGATCTACCTTCTGCTGAGAGAGTAAAG 365
300 GCAGATTCAGAGAGAGCTGCGACCTCCGGAGCATGAGAGAGTGAAGTGTCTGAG 359
366 GCGATTTCTTAAAGATCAACCTGTGTAAACAGAGCGGCGAAATGCTGCTGAG 425
360 CACCTTGAAGAGAGAGCTGCGACCTTGTGTGAGTGGGAAATGCTGAGAGCCCTCG 419
426 CACCTTGAAGAGAGAGCAATGCGCTCTGGGATGAGAGAGATGTTGCTGAGAGCCCTAGA 485
420 GAGAACCGGAGAGCCCTCTGCGCCCGGCTACATGAACCTGAGACTCAAGACTTGGCCCTC 479
486 GCAAGATGGCAATCCCTTACGCGCGCTATGTCAACCACTCACTGATGTGCTGCTC 545
480 TCCATGTTTGAAGAGAGCTCATGATGAATCTCAACTGCTGAGACTCTCTCAGCCAC 539
546 TCTTCTCTGAGAGCTGCGCATGAGATGTCTCCACTTGTCTGAGAGCCCTCTCAGCCAC 605
540 TCTGTGAGAGAGCTTCTGATGAGAGCTCTTGAATGATGAGAGAGAGAGTGT 599
606 TTTGGTGAAGAACTTCTGATTAACATGCTTGAACATCTGCTTGAAGAGAGCTAAT 665
600 GACATTTGAAGAGAGAACTCGGATGCTGCTGAGAGAGAGAGAGAGATGATGATG 659
666 GACAGTGAAGAGAGAGAACTCGGATGCTGCTGAGAGAGAGAGAGAGATGATGATG 725
660 AAGAGAGCTACTAAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
726 AAGAGAGCTGCTGAGAGAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 785

720 TCTTGTGAAGACAGAGAAACAATGAATCTGTCCAGAGTAAACAGGCTGATGTGCTCAGA 779
786 TTTGGCCCAATGTGAAGATGATGCTATTTCCAGAGAACTTACAGGTGAGAGCTGCCAGA 845
780 AAGCAATGAGAGATGAGAAATTTATCAAGATTGATGCTCTCAAGTGAAGAGCAACT 839
846 AGACAACAGAGCTTGGCTAACTGCTCAAGAGATGGGCTGAGCTGAATGATGATGCT 905
840 TCTTTCACACAGTTCAAGCCAAATCTGAGAGAGAGAGTCTGGGCGATGAGAAATACCTC 899
906 TCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965
900 ATCAGATCAATCTTTGAGAGATCTCTGATGATGATGATGATGATGATGATGATGATG 959
966 ACCAGAGGCTTTTATGAGATGCTCTGATGATGATGATGATGATGATGATGATGATG 1025
960 AGGAAGTGCAGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1019
1026 AGGAAGTGCAGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1085
1020 AGGACCATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1076
1086 AGGACCATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1145
1077 GCCAGATCTCCAGCTCAGGCTTACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
1146 GCCAGATCTCCAGCTCAGGCTTACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205
1137 GAATATCATCTGCTCTCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1196
1206 GAATATCATCTGCTCTCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
1197 CAAGATCATCTTGAAG 1256
1266 CAAGATCATCTTGAAG 1325
1257 CAATAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1316
1326 CAATAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1385
1317 ATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1376
1386 ATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1445
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1437 CTGAG 1496
1506 TCTGAG 1565
1497 TGAATGATCATCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1556
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1557 GCAG 1616
1626 GCAG 1685
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1737 AAGATCTGATCAATGAG 1796
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Db      1866  TGAACACAGAGAAAATCCATTTAAAGAAAATTTAGAAATTTATGCGACGATTCAGAC 1925
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Db      3183  AATTAAGAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3242
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RESULT 15
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XX      XX
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KW      ligase; hyperproliferative disorder; immunodeficiency disorder;
KW      autoimmune disorder; neurological disorder; metabolic disorder;
KW      inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW      blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW      anti-rheumatic; nephrotoxic; anticoagulant; ss.
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PD      02-AUG-2001.
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PF      17-JAN-2001; 2001WO-US001239.
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PR      24-FEB-2000; 2000US-0184664P.
PR      02-MAR-2000; 2000US-0186350P.
PR      16-MAR-2000; 2000US-0189874P.
PR      17-MAR-2000; 2000US-0190076P.
PR      18-APR-2000; 2000US-0198123P.
PR      19-MAY-2000; 2000US-0205515P.
PR      07-JUN-2000; 2000US-0209467P.
PR      28-JUN-2000; 2000US-0214886P.
PR      30-JUN-2000; 2000US-0215135P.
PR      07-JUL-2000; 2000US-0216647P.
PR      07-JUL-2000; 2000US-0216880P.
PR      11-JUL-2000; 2000US-0217487P.
PR      11-JUL-2000; 2000US-0217496P.
PR      14-JUL-2000; 2000US-0218290P.
PR      26-JUL-2000; 2000US-0220963P.

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CC invention can also be used in gene therapy. AAS40785-AAS41684 represent
 CC cDNA sequences encoding for the novel human enzyme polypeptides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1967 BP; 723 A; 344 C; 416 G; 476 T; 0 U; 8 Other;

Query Match 55.8%; Score 1878; DB 4; Length 1967;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1941; Conservative 5; Mismatches 18; Indels 7; Gaps 5;

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QY	1107	GGAAGTTGGCCAGCCGCTTGGAGAGGAAATATCATCTGCTCTCTACAGGGAG	1166
DB	62	GGAAGTTGGCCAGCCGCTTGGAGAGGAAATATCATCTGCTCTCTACAGGGAG	121
QY	1167	TGGAAGAAACAGAGTGGCTGTTTACATTCGCAAGATCACTTACAGAGAGAGAAAGC	1226
DB	122	TGGAAGAAACAGAGTGGCTGTTTACATTCGCAAGATCACTTACAGAGAGAGAAAGC	181
QY	1227	ATCTGAGCTGGAGAAAGTTAATGTTCTTGTCAATAAGTAAGTCTAAGTGAACGCTCTT	1286
DB	182	ATCTGAGCTGGAGAAAGTTAATGTTCTTGTCAATAAGTAAGTCTAAGTGAACGCTCTT	241
QY	1287	CCGCAAGAGGTTCCACATTTTGAAGAAATGCTATCGTGTATTGGATTAAAGTGTGA	1346
DB	242	CCGCAAGAGGTTCCACATTTTGAAGAAATGCTATCGTGTATTGGATTAAAGTGTGA	301
QY	1347	TACCCAACTGAGAAATATCATTTCCAGAGTGTCAAGTCTGTGATTAATATCAGTAC	1406
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QY	1407	AGCTCAAAATCTTGAAGAACTCCCTCTTAAACTTGAAGAAATGAGAGATGCTGTGTGA	1466
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QY	1467	ATTGTGAGCTTTTCCCTCATTTATCATTTGATGATGTCATCACACCAAGAGAGAGCT	1526
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QY	2127	TTGTGATGCTGATGAAGATGAGATGATTTTAAAGAACTTTGAAACTGATGAAACAG	2186
DB	1082	TTGTGATGCTGATGAAGATGAGATGATTTTAAAGAACTTTGAAACTGATGAAACAG	1141
QY	2187	TGATTTTCTCATGACTTATTTTGAAGAAATGTTGAAGAGCTGGCTGAGAA	2246
DB	1142	TGATTTTCTCATGACTTATTTTGAAGAAATGTTGAAGAGCTGGCTGAGAA	1201
QY	2247	CCAGAAATGAGAAATGAGAAAGCTGACCAATTAAGAAATACATATATGAGCAATATAC	2306
DB	1202	CCAGAAATGAGAAATGAGAAAGCTGACCAATTAAGAAATACATATATGAGCAATATAC	1261
QY	2307	TGAGCTGAGATGACGACGAGAAATATCTTTTCAAAAACAGACAGATGCTATATGC	2366
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DB	1382	TCTGATGAGCTGACACAGAGAGTGAATCAACCCATGACACAGAAATGAACAAAGAA	1441
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QY	2727	GATGTTAAAGCTATATCATTTGTTCAAAATATGAAACCAAGAGATATGCTCATATGAT	2786
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1393	41.4	2304	4 AK037057	AK037057 Mus muscu
4	1367.4	40.6	2331	4 AK040519	AK040519 Mus muscu
5	926.4	27.5	1013	3 BQ233683	BQ233683 AGENCOURT
6	900.4	26.8	1174	5 BU902097	BU902097 AGENCOURT
7	806.8	24.0	1115	5 BQ467983	BQ467983 AGENCOURT
8	801.8	23.8	870	5 BQ960157	BQ960157 AGENCOURT
9	728.2	21.6	918	5 BU189982	BU189982 AGENCOURT
10	718.8	21.4	755	5 BQ772836	BQ772836 UT-H-PEO-
11	711.6	21.1	1035	2 BF337464	BF337464 602035195
12	687	20.4	729	2 BF983236	BF983236 602305873
13	680.4	20.2	690	8 DR422160	DR422160 nav08905.
14	654.4	19.4	701	6 CA423868	CA423868 UT-H-FEL-
15	652.8	19.4	827	2 BG741146	BG741146 602631817
16	651.8	19.1	781	2 BF686405	BF686405 602143786
17	641.8	19.1	653	7 CR752055	CR752055 DKFZ0469M
18	626	18.6	1046	3 BM476961	BM476961 AGENCOURT
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20	622.4	18.5	1041	2 BE882040	BE882040 601505326
21	618.4	18.4	1197	4 AK018602	AK018602 Mus muscu
22	616.2	18.3	1239	3 BM467774	BM467774 AGENCOURT

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27	596.8	17.7	619	3 BQ016388	BQ016388 UT-H-DT1-
28	584	17.4	1611	3 BM455238	BM455238 AGENCOURT
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31	551.2	16.4	568	3 BQ311714	BQ311714 QV3-BN004
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VERSION DQ050960.1 GI:66904159
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Homidae; Homo.
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Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Clevello,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ex) PLOS Biol. 3 (6), E170 (2005)
JOURNAL PUBLISHED 15869325
REFERENCE 2 (bases 1 to 3078)
Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Clevello,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submision
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
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Db 61 AGGGTGAATAATGTAATCCAGGTGGAGCTGTCTGTGATCACTGACCTTTCTGCTGCA 120
QY 289 GAGGTGAAGAGAGATTCCAGAGACAGTGGCCACCTCCGGGAAATGACGAGGATTTGA 348
Db 121 GAGGTGAAGAGAGATTCCAGAGACAGTGGCCACCTCCGGGAAATGAGGAGTTGA 180
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QY 769 GATTGCTCAGAAACCAATGAGATTTGAGATTTTATCACAAGTTGATGCTCTCAAGT 828
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Db 661 GAAGACCACTTTTCAACACAGTTCAAGCAAAATCTGAGAAAGAGGCTGTGGGCAATG 720
QY 889 GAGATTAATCTCATCAGATCATCTTTTGCAGATTTCTTGTAGTTTCAAGATCAGACACA 948
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QY 949 AGTTTGGCAGAGAAAGTGTCACTGCTGTTAGTGAAGTCTTGTGACATTAACAGCAATG 1008
Db 781 AGTTTGGCAGAGAAAGTGTCACTGCTGTTAGTGAAGTCTTGTGACATTAACAGCAATG 840
QY 1009 GGGAGGATTCAGAGCAATGGAGAGTTTCAAGTGAAGAGAAATGTGGAGCAAGGCA 1068
Db 841 GGGAGGATTCAGAGCAATGGAGAGTTTCAAGTGAAGAGAAATGTGGAGCAAGGCA 900
QY 1069 TCCCGGAGCCAGAACTCCAGCTCAGGCTTACCAATGGAAGTTGCCAGCCAGCTTGT 1128
Db 901 TCCCGGAGCCAGAACTCCAGCTCAGGCTTACCAATGGAAGTTGCCAGCCAGCTTGT 960
QY 1129 GAAAGGAAGAAATATCATCATCTGCTCTCTTAAGAGAGTGGAAACCAAGTGGCTGTT 1188
Db 961 GAAAGGAAGAAATATCATCATCTGCTCTCTTAAGAGAGTGGAAACCAAGTGGCTGTT 1020
QY 1189 TAATTTGCCAAGATCACTTAAGACAGAAAGAAACCAATCTGAGCCTGGAAGAAATATA 1248
Db 1021 TAATTTGCCAAGATCACTTAAGACAGAAAGAAACCAATCTGAGCCTGGAAGAAATATA 1080

QY 1249 GTTCTTGTCAATTAAGTACTGCTAGTTGAACAGCTTTTCCGAGAGAGTTCCACCATTT 1308
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QY 1669 AAAGCTGAAGAACACATTTTAAACCTATGAGCAATCTTGATGCAATTTACTATTAAACT 1728
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QY 1849 ATTCAAACTTAATGTCAAAAATGAGTCCAAATGTCAGATTTTGAACCTCAATGAACA 1908
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QY 1909 TGGGCAATTCAAATGAAAAAAGCTGCAAAAAAAGAAATCGCAAGAACGTGTTGT 1968
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QY 2029 GATGCGTATATCAATCTTGAACCTTCTTAATGAAGAGAAATGAAGTTTGCAGTC 2088
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Db 1921 ATAGAAGATGATGATGATGAGGCTGTGTGATGATGATGATGATGATGATGATGATGATG 1980
QY 2149 GATGATTTAAAGAAACCTTTGAACCTGATGAAACAGATTAATGATTTCTCATGACTTTATTT 2208
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OY	2389	AATGAAAAATTTGCTGAGTAGAGAGTCAAAAGCCCACTATCTGATTTGAGCTGCACAGC	2448
Db	2221	AATGAAAAATTTGCTGAGTAGAGAGTCAAAAGCCCACTATCTGATTTGAGCTGCACAGC	2280
OY	2449	AGTGAATTCAAAACCATGACACAGATGAACAAAAAGAGTCATTAGTAAATTTCCGACT	2508
Db	2281	AGTGANNNNNNNNNNNNNNNNNNNNNAATGAACAAAAAGAGTCATTAGTAAATTTCCGACT	2340
OY	2509	GGAAAAATCAATCTGCTTATGCTTACCAACAGTGGCAAGAAAGGCTGAGATTTAAGAA	2568
Db	2341	GGAAAAATCAATCTGCTTATGCTTACCAACAGTGGCAAGAAAGGCTGAGATTTAAGAA	2400
OY	2569	TGTAAACATGTTATCCGTTATGTCGTCAACCAATGAATAAGCAATGTCACAGGCCGT	2628
Db	2401	TGTAAACATGTTATCCGTTATGTCGTCAACCAATGAATAAGCAATGTCACAGGCCGT	2460
OY	2629	GGTCGAGCCAGAGCTGATGAGAGCACCTACGCTCGTGTGCTCACAGTGGTTCAGAGTT	2688
Db	2461	GGTCGAGCCAGAGCTGATGAGAGCACCTACGCTCGTGTGCTCACAGTGGTTCAGAGTT	2520
OY	2689	ATCGAACATGAGACGTTAATGATTTCCGAGAGAAAGATGATGTAAAGCTTACATGTT	2748
Db	2521	ATCGAACATGAGACGTTAATGATTTCCGAGAGAAAGATGATGTAAAGCTTACATGTT	2580
OY	2749	GTTCAAAATATGAAAACGAGAGAGTATGCTCATTAAGATTTTGGAAATTACAGTCAAAAGT	2808
Db	2581	GTTCAAAATATGAAAACGAGAGAGTATGCTCATTAAGATTTTGGAAATTACAGTCAAAAGT	2640
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OY	2869	TCACATAATACCTTCTCTTGGCAAAAACGCAAGTGTGTAGCGCTGTTCTGGGGAAGATATC	2928
Db	2701	TCACATAATACCTTCTCTTGGCAAAAACGCAAGTGTGTAGCGCTGTTCTGGGGAAGATATC	2760
OY	2929	CATGTAATTGAGAAAATGCATCACGTCATATATGACCCCGAGATTCAGAGAACTTTACATT	2988
Db	2761	CATGTAATTGAGAAAATGCATCACGTCATATATGACCCCGAGATTCAGAGAACTTTACATT	2820
OY	2989	GTAAGAGAAAACAAAGCACTGCAAAAAGAAAGTGTGCCGACTATCAATTAATGTGGAATC	3048
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OY	3049	ATTCGCAATGTGGCCAGAGCTTTGGGGAACAATGAATGTGCACAAAAGCTTGAATTTGGCT	3108
Db	2881	ATTCGCAATGTGGCCAGAGCTTTGGGGAACAATGAATGTGCACAAAAGCTTGAATTTGGCT	2940
OY	3109	TGTCCTCAAAATPAAGAAATTTGTAGTGTGTTTTCAAAATTAATTCACAAAGAAACAATAC	3168
Db	2941	TGTCCTCAAAATPAAGAAATTTGTAGTGTGTTTTCAAAATTAATTCACAAAGAAACAATAC	3000
OY	3169	AAAAAGTGGTAGAATTAACCTATCAATCTTCCCAATCTTGAATTCAGAAATGCTGTTA	3228
Db	3001	AAAAAGTGGTAGAATTAACCTATCAATCTTCCCAATCTTGAATTCAGAAATGCTGTTA	3060
OY	3229	TTTAGTATGATGAGATTTAG 3246	
Db	3061	TTTAGTATGATGAGATTTAG 3078	

RESULT 2					
DQ050961	DQ050961	3078 bp	DNA	linear	GSS 02-JUN-2005
LOCUS	Pan troglodytes MDAs gene, VIRtUAL TRANSCRIPT, partial sequence,				
DEFINITION	genomic survey sequence.				
ACCESSION	DQ050961				
VERSION	DQ050961.1	GI:66904160			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				

ORGANISM	Pan troglodytes	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eumetaria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE	1 (bases 1 to 3078)	2 (bases 1 to 3078)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.U., Smithy,J.J., Adams,M.D. and Cargill,M.	Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.U., Smithy,J.J., Adams,M.D. and Cargill,M.
TITLE	A scan for positively selected genes in the genomes of humans and chimpanzees	
JOURNAL	(er) Plos Biol. 3 (6), E170 (2005)	
REFERENCE	15669325	
AUTHORS	2 (bases 1 to 3078)	
TITLE	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.U., Smithy,J.J., Adams,M.D. and Cargill,M.	
JOURNAL	Direct Submission	
COMMENT	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
FEATURES	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	
source	location/Qualifiers	
gene	1..3078	
ORIGIN	/organism="Pan troglodytes"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9598"	
	<1..>3078	
	/gene="MDA5"	
	/locus_tag="HC18981"	
Query Match	85.0%; Score 2861; DB 11; Length 3078;	
Best Local Similarity	93.1%; Pred. No. 0;	
Matches 2867; Conservative	0; Mismatches 211; Indels 0; Gaps 0	
169	ATGTGGAATGGGTATTCACAGAGAGAAATTTCCGCTATCTCATCTGCTTCAGGGCC	228
1	ATGTGGAATGGGTATTCACAGAGAGAAATTTCCGCTATCTCATCTGCTTCAGGGCC	60
229	AGGGTGAATATGTCATCAGGTGGAGCTGTGGCTGGAATTCAGCTTCTGCTGCA	288
61	AGGGTGAATATGTCATCAGGTGGAGCTGTGGCTGGAATTCAGCTTCTGCTGCA	120
289	GAGGTGAAGAGCAGATTCAAGAGCAGTCCGCCATTCGCGGAAATCATGAGGCACTTGA	348
121	GAGGTGAAGAGCAGATTCAAGAGCAGTCCGCCATTCGCGGAAATCATGAGGCACTTGA	180
349	CTGCTGTAGACACCTTGGAGAGGAGTCTGGCACTTGTGTGAGCTTCGGAATTCGTG	408
181	CTGCTGTAGACACCTTGGAGAGGAGTCTGGCACTTGTGTGAGCTTCGGAATTCGTG	240
409	GAGGCTCTCGGAGAACCGGAGCCCTTGGCCGCGCGCTACATGAACCTGAGGCTCAG	468
241	GAGGCTCTCGGAGAACCGGAGCCCTTGGCCGCGCGCTACATGAACCTGAGGCTCAG	300
469	GACTTGCCTCTGCATCGTTTGAGAGCGCTATGATGAATATCTTCAACTGCTGAACCTC	528
301	GACTTGCCTCTGCATCGTTTGAGAGCGCTATGATGAATATCTTCAACTGCTGAACCTC	360
529	CTTCAAGCCACTCTGTGTGAGCAAGCTTCTAGTGAAGAGCTTGTGATGAAGTCAATGAG	588
361	CTTCAAGCCACTCTGTGTGAGCAAGCTTCTAGTGAAGAGCTTGTGATGAAGTCAATGAG	420
589	GAGGAACGTGTGAACAATTGAAGAGCAAAACCGGAAATGTGCTGCGAGAAACCAATGGAAT	648
421	GAGGAACGTGTGAACAATTGAAGAGCAAAACCGGAAATGTGCTGCGAGAAACCAATGGAAT	480
649	GAATCAGGTGTGAAGAGCTATAAAGATTGTGCAAGAAAGAAATCTGTTCTCTGCA	708
481	GAGTCAGGTGTGAAGAGCTATAAAGATTGTGCAAGAAAGAAATCTGTTCTCTGCA	540
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Db 541 TTCTGAATGTTCTGTCAACAGAAACAATGAATCTGTCCAAAGTTAAACAGCTCT 600
769 GATGTGTCGAAGAAGCAATGAGAGATTGGAATTTATCAACAATTGATGCTCTCAAGT 828
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Db 601 GATGTGTCGAAGAAGCAATGAGAGATTGGAATTTATCAACAATTGATGCTCTCAAGT 840
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661 NNN 720
Qy 889 GAGAAATACATCATCAGATCATCTTTTGCAGATTCTTCTGAGTTTCAGATCAGACACA 948
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901 TCCCGGAGCCAGAACTCCAGCTCAGGCTTACCAAATGGAAGTTGCCAGCCACTTG 960
Qy 1129 GAAGGAGAAATTCATCATCTGCTCCCTACAGGGAGTGGAAAAACAAGTGGCTTT 1188
961 GAAGGAGAAATTCATCATCTGCTCCCTACAGGGAGTGGAAAAACAAGTGGCTTT 1020
Db 1189 TACATTGCCAAGATCACTTAGACAAGAGAAAAAGCATCTGAGCTTGAAAAAGTTATA 1248
1021 TACATTGCCAAGATCACTTAGACAAGAGAAAAAGCATCTGAGCTTGAAAAAGTTATA 1080
Qy 1249 GTTCTTGTCAATAAGTACTGCTAAGTTGAAACAGCTCTTCCGCAAGAGTTCCAACTTT 1308
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Qy 1309 TTGAAGAAATGATGATGCTGTTATTGGAATTAAGGGGATACCAACTGAAATATCTTT 1368
1141 TTGAAGAAATGATGATGCTGTTATTGGAATTAAGGGGATACCAACTGAAATATCTTT 1200
Qy 1369 CCAGAAGTTGTCAAGTCTGTGATATTTATATCATGATCAGCTCAAACTCTTGAAAACTCC 1428
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Qy 1429 CTCTTAACTTGGAAAAATGAGAAAGATGCTGTGTTCAATTGTCAGACTTTTCCCTCAT 1488
1261 CTCTTAACTTGGAAAAATGAGAAAGATGCTGTGTTCAATTGTCAGACTTTTCCCTCAT 1320
Qy 1489 ATCATTTGATGAATGATCATCACCAACAAGAGAGTGTATTAATTAATCATCATGAGGCAT 1548
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Qy 1549 TATTTGATGAGAGAGTTGAAAAACAATAGACTCAAGAAAAAACAACCAAGTATTTCCC 1608
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1441 CTTCCTCAGATCTGGGACTTAACAGCTTCACTGTGTGAGAGGGCCACGAAACAGCC 1500
Qy 1669 AAAGCTGAGAGAACATTTTAAAACTATGTGCCAATCTTTGATGATTTATTAATAAAT 1728
1501 AAAGCTGAGAGAACATTTTAAAACTATGTGCCAATCTTTGATGATTTATTAATAAAT 1560
Qy 1729 GTTAAAGAAAACTTGTATCACTGAAAAACAATAAGAGAGCCATCAAGAAATTTGCC 1788
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Qy 1789 ATTGCAGATCAACAGAGAAAGATCAATTTAAAGAAATCTTCTAGAAATATGACAGG 1848
|||||

Db 1621 ATTGCAGATCAACAGAGAAAGATCCATTTAAAGAGAACTNNNAGAAATATGACAGG 1680
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Db	2821	GTAAGAGAAAACAAAGCAGTCGCAAAAGAGTGTGTCCGACTATCAATTAATAGTGAATC	2880
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Qy	3169	AAAAAGTGGTAGAATTAACCTATCAATCCATCTTGACTATTCAGAAATGCTGTTTA	3228
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Qy	3229	TTTAGTGTATGAGATTAG	3246
Db	3061	TTTAGTGTATGAGATTAG	3078
RESULT 3			
AK037057			
LOCUS			
DEFINITION	AK037057	2304 bp	mRNA linear HTC 03-APR-2004
	Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930105B04 produce:similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens], full insert sequence.		
ACCESSION	AK037057.1	GI:26331913	
VERSION			
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	1		
TITLE	Carninci, P. and Hayashizaki, Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
PUBMED	Meth. Enzymol. 303, 19-44 (1999)		
REFERENCE	10349636		
AUTHORS	2		
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
PUBMED	Genome Res. 10 (10), 1617-1630 (2000)		
REFERENCE	11042159		
AUTHORS	3		
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Teshiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Onara, E., Wataniki, M., Yokozaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)		
REFERENCE	11076861		
AUTHORS	4		
TITLE	THE RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
PUBMED	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	THE PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		

TITLE Analysis of the mouse transcriptome based on functional annotation
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2304)
AUTHORS Aachii,T., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagasaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hitamoto,K., Hiraoka,T., Hirozane,T., Horii,P., Imctani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komio,H., Kouda,M., Koya,S., Kuhihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Saeki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,P., Takara-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yaeunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
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ORIGIN
Query Match 41.4%; Score 1393; DB 4; Length 2304;
Best Local Similarity 79.3%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 435; Indels 7; Gaps 3;
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RESULT 4
AK040519
LOCUS AK040519 2331 bp mRNA linear HTC 03-APR-2004

DEFINITION	Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430105A06 product:similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 (Homo sapiens), full insert sequence.
ACCESSION	AK040519
VERSION	AK040519.1 GI:26333792
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y.
AUTHORS	High-efficiency full-length cDNA cloning
TITLE	Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	10349636
PUBMED	2
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
TITLE	Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	11042159
PUBMED	3
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
AUTHORS	RIKEN integrated sequence analysis (RISA) system-384-format
TITLE	Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL	11076861
PUBMED	4
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
AUTHORS	Functional annotation of a full-length mouse cDNA collection
TITLE	Nature 409, 685-690 (2001)
JOURNAL	5
PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
TITLE	Nature 420, 563-573 (2002)
JOURNAL	6 (bases 1 to 2331)
PUBMED	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kashiwagi, K., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyas, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeida, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
AUTHORS	Direct Submission
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, url:ftp://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
JOURNAL	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
COMMENT	

Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
Location/Qualifiers

FEATURES

source

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CDS

ORIGIN

Query Match 40.6%; Score 1367.4; DB 4; Length 2331;
Best Local Similarity 79.2%; Pred. No. 0;
Matches 1663; Conservative 0; Mismatches 431; Indels 7; Gaps 3;

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DB 2331 C 2331

RESULT 5
BQ233683 1013 bp mRNA linear EST 02-MAY-2002
LOCUS AGENCOURT_7258428 NIH_MGC_71 Homo sapiens cDNA IMAGE:5786526
DEFINITION 5', mRNA sequence.
ACCESSION BQ233683
VERSION BQ233683.1 GI:20415083
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1013)
REFERENCE 1 NIH-MGC <http://mgi.mgi.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12875 row: 9 column: 07
High quality sequence stop: 721.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="IMAGE:5786526"
/cisue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_71"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb. "

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ORIGIN

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Query Match      27.5%; Score 926.4; DB 3; Length 1013;
Best Local Similarity 98.3%; Pred. No. 8.4e-215;
Matches 989; Conservative 0; Mismatches 11; Indels 6; Gaps 5;

QY 1752 GAAAAACCAATCAGAGCCATGCAAGAGTTGGCCATTGCGAGTCAACGAGAGAGA 1811
    1 GAAAAACCAATCAGAGCCATGCAAGAGTTGGCCATTGCGAGTCAACGAGAGAGA 60
QY 1812 TCCATTTAAAGAGAACTCTAGAAATATGACAGAGATTCAACTTATTGTCAATGAG 1871
    61 TCCATTTAAAGAGAACTCTAGAAATATGACAGAGATTCAACTTATTGTCAATGAG 120
QY 1872 TCCAAATGTCAGATTTTGGAACTCAACCTTATGAACAATGGCCATTCAAAATGGAAGAAA 1931
    121 TCCAAATGTCAGATTTTGGAACTCAACCTTATGAACAATGGCCATTCAAAATGGAAGAAA 180
QY 1932 AGCTGCAAAAAGAAAGAAATCGCAAGAAACGTTTGTGAGAGCAATTGAGAGATCA 1991
    181 AGCTGCAAAAAGAAAGAAATCGCAAGAAACGTTTGTGAGAGCAATTGAGAGATCA 240
QY 1992 TGAGGCCCTCAAAATTAATGACAAATTCGAATGATGATCGTATATCTCATCTTGAAC 2051
    241 TGAGGCCCTCAAAATTAATGACAAATTCGAATGATGATCGTATATCTCATCTTGAAC 300
QY 2052 TTTCTTATGAGAGAGAAATGAAGTTTGCAGTCATGGAAGATGATGATGAGG 2111
    301 TTTCTTATGAGAGAGAAATGAAGTTTGCAGTCATGGAAGATGATGATGAGG 360
QY 2112 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2171
    361 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 2172 ACTGATGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2231
    421 ACTGATGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 2232 AAGGCTGGCTGAAACCCAGAAATATGAAAGCTGACCAATTAAGAAATACAT 2291
    481 AAGGCTGGCTGAAACCCAGAAATATGAAAGCTGACCAATTAAGAAATACAT 540
QY 2292 AATGAGCAATATATGAGCTGAGAGAAATGACACGAGAAATATCTTACAAACACG 2351
    541 AATGAGCAATATATGAGCTGAGAGAAATGACACGAGAAATATCTTACAAACACG 600
QY 2352 ACAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2411
    601 ACAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 2412 AGTCAAGCCACCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2471
    661 AGTCAAGCCACCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 2472 GAATGAACAAAGAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2531
    721 GAATGAACAAAGAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 2532 TACCAAGTGGCAGAGAAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2591
    781 TACCAAGTGGCAGAGAAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 2592 TCTGTCACCAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2651
    841 TCTGTCACCAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899

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QY 2652 CACCTACGTCCTGTTGCTCAGAGTTCAGAGATTAATGAAATGAGACAGTTATGA 2711
    900 CACCTACGTCCTGTTGCTCAGAGTTCAGAGATTAATGAAATGAGACAGTTATGA 956
QY 2712 TTTCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2757
    957 TTTCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1000

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RESULT 6
BU902097 1174 bp mRNA linear EST 17-OCT-2002
LOCUS AGENCOURT 10127740 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5602757
DEFINITION 5', mRNA sequence.
ACCESSION BU902097
VERSION BU902097.1 GI:24084010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

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REFERENCE 1 (bases 1 to 1174)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

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FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5602757"
/cisue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb. "

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ORIGIN

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Query Match      26.8%; Score 900.4; DB 5; Length 1174;
Best Local Similarity 93.7%; Pred. No. 2e-208;
Matches 1049; Conservative 0; Mismatches 56; Indels 15; Gaps 10;

QY 1 GCGCGCGGCTGAGAGCCCTGTCGCAACCTCGTATGTCAGGACAGAGGGGTAGAC 60
    55 GCGCGCGGCTGAGAGCCCTGTCGCAACCTCGTATGTCAGGACAGAGGGGTAGAC 114
QY 61 CCGCTTCTTAAGTGGAGAGCGGACAGGACAGGACATTTCACTGTCGCGACAGCA 120
    115 CCGCTTCTTAAGTGGAGAGCGGACAGGACAGGACATTTCACTGTCGCGACAGCA 174
QY 121 CAGCACATCTGCTGGAGAACCTCTCTCTCTGAGAAAGAAAGATGTCGAATGG 180
    175 CAGCACATCTGCTGGAGAACCTCTCTCTCTGAGAAAGAAAGATGTCGAATGG 234
QY 181 TATTCACAGAGAAATTTCCGCTATCTCATCTGCTTCAAGGCGCAGGGGGAATG 240
    235 TATTCACAGAGAAATTTCCGCTATCTCATCTGCTTCAAGGCGCAGGGGGAATG 294
QY 241 TACATCAGGTGAGGCTGTGCTGACTGACTGACTTCTGCTGCTGAGAGTGAAGAG 300

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Db 295 TACATCCAGGTGAGCCTGTGCTGAGACTACCTGACCTTTCTGCTGCAGAGTGAGAG 354
Qy 301 CAGATTCAAGAGAGCAGTCCGACCTCCGGGAGCATGACGAGCAGTTGAATGCTGTGAGC 360
Db 355 CAGATTCAAGAGAGCAGTCCGACCTCCGGGAGCATGACGAGCAGTTGAATGCTGTGAGC 414
Qy 361 ACCTTGAGAGAGGAGTCTGAGCCTTTGTTGACTCGGAAATTCGTGAGGCCCTCCGG 420
Db 415 ACCTTGAGAGAGGAGTCTGAGCCTTTGTTGACTCGGAAATTCGTGAGGCCCTCCGG 474
Qy 421 AGAACCGGACGCTCTGAGCCCGCCGCTACATGAACTTGAAGCTCAAGAGCCTTCCCTC 480
Db 475 AGAACCGGACGCTCTGAGCCCGCCGCTACATGAACTTGAAGCTCAAGAGCCTTCCCTC 534
Qy 481 CCATCGTTGAGAGACGCTCATGATGATATCTCAACTGCTGAACTCTTCAAGCCACT 540
Db 535 CCATCGTTGAGAGACGCTCATGATGATATCTCAACTGCTGAACTCTTCAAGCCACT 594
Qy 541 CTGGTGAACAAGCTTTAGTTAGAGACGCTTGGATTAAGTCATGAGAGAGAACTGTTG 600
Db 595 CTGGTGAACAAGCTTTAGTTAGAGACGCTTGGATTAAGTCATGAGAGAGAACTGTTG 654
Qy 601 ACAATTGAAAGACGAAACCGGAGTTGCTGCTGCAGAAACAAATGGAATGAATCAGGTGA 660
Db 655 ACAATTGAAAGACGAAACCGGAGTTGCTGCTGCAGAAACAAATGGAATGAATCAGGTGA 714
Qy 661 AGAGAGCTACTAAAGAGATTGTGACAGAAAGAAACCTGTTCTGTGACTTCTGAATGTT 720
Db 715 AGAGAGCTACTAAAGAGATTGTGACAGAAAGAAACCTGTTCTGTGACTTCTGAATGTT 774
Qy 721 CTTCGTCAACAGAGAAACAATGAATCTTGTCAAGAGTTAAACAGGCTCTGATTCCTCAGAA 780
Db 775 CTTCGTCAACAGAGAAACAATGAATCTTGTCAAGAGTTAAACAGGCTCTGATTCCTCAGAA 834
Qy 781 AGCAATGACAGAGATTGAATTTATCAACAAGTTGATGCTCAAGT-GGAAGAGCAACT 839
Db 835 AGCAATGACAGAGATTGAATTTATCAACAAGTTGATGCTCAAGTGGGAGAAAGCAACT 894
Qy 840 TCTTTTCAACACA-GTTCAAGCCAAATCTGG-AGAGAGAGGTCTGGGGCATGG-AGATAA 896
Db 895 TCTTTTCAACACAAGTTCAAGCCAAATCTGGAGAAAGAGGTCTGGGGCATGGAGAAATTA 954
Qy 897 CTCATC-AGAAATCATCTTTTGGAGATTTCTTCTGATGTTCAAGATCAGACACAAGTTGG 955
Db 955 CTCATCAAAATCATCTTTTGGAGATTTCTTCTGAGTTCAAGAACCAAAATGTTGGG 1014
Qy 956 C-AGAGAGAGGTCTGAGTCTT-AGATGAAGTCTT-GGACATTAACAGCAATGGGCA 1012
Db 1015 CAAAAAGAAATGCAACTGCTTAAATGAAGTCTTGGGACATTAACAAACATGGGCA 1074
Qy 1013 GTGATTCAAGCACCATGGG--AAGTGAATTCAGATGAAGAAATGTGGCAGCAAGACA- 1068
Db 1075 GGGATTTCCGGCCCCCGGGGCAAAAGATTTCAAAATTAATAAAGGGGCCAACCAAGAAA 1134
Qy 1069 ---TCCCCGGAGCCAGAACTCAAGCTCAAGGCTTTACCAA 1105
Db 1135 ATTCGCCGGGAACAAAAAATTCAGCTTGGGCCCTTAACAA 1174

RESULT 7
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LOCUS Bm467983 AGENCOURT 6437921 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532884
DEFINITION 5' mRNA Sequence.
ACCESSION Bm467983
VERSION Bm467983.1 GI:18517025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1115)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM12216 Row: n Column: 21
High quality sequence stop: 690.
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1. 1115
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/clone="IMAGE:5532884"
/issue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 Kb."

ORIGIN
Query Match 24 0%; Score 806.8; DB 3; Length 1115;
Best Local Similarity 99.6%; Pred. No. 1.5e-185;
Matches 808; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2555 TGGATATTAAGATGTAACATTTGTTATCGTTATGCTGTCACCAATGAATAGCCA 2614
Db 2 TGGATATTAAGATGTAACATTTGTTATCGTTATGCTGTCACCAATGAATAGCCA 61
Qy 2615 TGGTCAAGCCCGTGGTCAAGCCAGAGCTGATGAGACACTTACGCTCGTCTCACA 2674
Db 62 TGGTCAAGCCCGTGGTCAAGCCAGAGCTGATGAGACACTTACGCTCGTCTCACA 121
Qy 2675 GTGGTTCAAGAGTTATGCAACATGAGACAGTTAATGATTTCCGAGAGAGATGATATA 2734
Db 122 GTGGTTCAAGAGTTATGCAACATGAGACAGTTAATGATTTCCGAGAGAGATGATATA 181
Qy 2735 AAGCTATACATTGTGTTCAAATATGAAACAGAGAGATATGCTCATAGATTTGGAAT 2794
Db 182 AAGCTATACATTGTGTTCAAATATGAAACAGAGAGATATGCTCATAGATTTGGAAT 241
Qy 2795 TACAGATGCAAGTATATGAGAAAGAAATGAAACCAAGAGAAATTTGCCAGACTT 2854
Db 242 TACAGATGCAAGTATATGAGAAAGAAATGAAACCAAGAGAAATTTGCCAGACTT 301
Qy 2855 ACAAGAAATTAACCATCACTATATATCTTCTTGGCAAAAACTGACAGTGTGCTGTT 2914
Db 302 ACAAGAAATTAACCATCACTATATATCTTCTTGGCAAAAACTGACAGTGTGCTGTT 361
Qy 2915 CTGGGAGAGTATCATATGTAATGAGAAATGATCATGATGACCCAGAAATCA 2974
Db 362 CTGGGAGAGTATCATATGTAATGAGAAATGATCATGATGACCCAGAAATCA 421
Qy 2975 AGAAGCTTTACATTGTAAGAGAAACAAAGCACTGCAAAAAAGAGTGGCGATATCAAA 3034
Db 422 AGAAGCTTTACATTGTAAGAGAAACAAAGCACTGCAAAAAAGAGTGGCGATATCAAA 481
Qy 3035 TAAATGTAATCAATCTGCAATGAGTGGCAGGCTTGGGGAACAATGATGGTCACAAG 3094
Db 482 TAAATGTAATCAATCTGCAATGAGTGGCAGGCTTGGGGAACAATGATGGTCACAAG 541
Qy 3095 GCTTAATTTGCTGTCTCAAAATTAAGAAATTTGATGTTTCAAAAATTAATTCAA 3154
Db 542 GCTTAATTTGCTGTCTCAAAATTAAGAAATTTGATGTTTCAAAAATTAATTCAA 601
Qy 3155 CAAAGAAACATACAAAAAGTGGGTGAATTAACCTATACATTTCCCAATCTTGACTATT 3214

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L14M13546 row: a column: 17
 High quality sequence stop: 556.
 Location/Qualifiers

FEATURES

source

1. 918

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 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb."

ORIGIN

Query Match

Best Local Similarity 97.5%; Pred. No. 2,2e-166;
 Matches 814; Conservative 0; Mismatches 13; Indels 8; Gaps 7;

1245 TATAGTTCTTGTCAATPAGTACTGCTAGTTGAACAGCTTCCGCAAGAGTTCCAAAC 1304
 1 TATAGTTCTTGTCAATPAGTACTGCTAGTTGAACAGCTTCCGCAAGAGTTCCAAAC 60
 1305 ATTTTGAAGAAATGGATCGTTTATTTGATTAAGGTGATATACCACTGAAATATC 1364
 61 ATTTTGAAGAAATGGATCGTTTATTTGATTAAGGTGATATACCACTGAAATATC 120
 1365 ATTTCCAGAAAGTGTCAAGTCTGTGATATTTATTCAGTACAGCTCAATCTTGGAAA 1424
 121 ATTTCCAGAAAGTGTCAAGTCTGTGATATTTATTCAGTACAGCTCAATCTTGGAAA 180
 1425 CTCCTCTTAACTTGGAAAATGAGAAAGTGTGTTGATTTGTCAAGCTTTTCCCT 1484
 181 CTCCTCTTAACTTGGAAAATGAGAAAGTGTGTTGATTTGTCAAGCTTTTCCCT 240
 1485 CATTATCATTTGAGAAATGTCATCACACCAAGAAAGAGCTGATATATACATCATGAG 1544
 241 CATTATCATTTGAGAAATGTCATCACACCAAGAAAGAGCTGATATATACATCATGAG 300
 1545 GCATTAATTTGATCAGAAAGTTGAAAAACATAGACTCAAGAAAGAAACCAACAGTAT 1604
 301 GCATTAATTTGATCAGAAAGTTGAAAAACATAGACTCAAGAAAGAAACCAACAGTAT 360
 1605 TCCCTTCTCAGATACCTGGACTTAACAGCTTCACTGTGTGGAGGGCCACAGAGCA 1664
 361 TCCCTTCTCAGATACCTGGACTTAACAGCTTCACTGTGTGGAGGGCCACAGAGCA 420
 1665 AGCAAGCTGAGAAACATTTTAAACATATGTCACATCTTGATGATCTTCTATTTA 1724
 421 AGCAAGCTGAGAAACATTTTAAACATATGTCACATCTTGATGATCTTCTATTTA 480
 1725 AACTGTTAAAGAAACCTTGATCACTGAAACCAATACAGAGGCGATCAAGAAAGT 1784
 481 AACTGTTAAAGAAACCTTGATCACTGAAACCAATACAGAGGCGATCAAGAAAGT 540
 1785 TGCATTGCAAGATGCAACAGAGAAAGATCCATTTAAAGAGAACTTTAGAAATATGAC 1844
 541 TGCATTGCAAGATGCAACAGAGAAAGATCCATTTAAAGAGAACTTTAGAAATATGAC 600
 1845 AAGGATTTCAAACTTATTTGCAATGATGCAATGTCAGATTTTGGAACTCAACCTATGA 1904
 601 AAGGATTTCAAACTTATTTGCAATGATGCAATGTCAGATTTTGGAACTCAACCTATGA 660
 1905 ACAATGGG--CCATTCAATGAAAAA--GCTGCAAAAAAAGAAATGCAAGAAAGC 1961
 661 AATATGGGCCCATTTCCAAATGAAAAAAGGCGTGGCAAAAGAAATGGCAAGAACG 720
 1962 TG-TTTGTGCAAAACATTTGAGAAAGTACATG-AGGCCCTTCAAAATT-AATGACACAT 2018
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Db 721 TGTTTTGCAAAAACCTTTGAGAAAGTACATGAAAGCCCTTACAAATTAATGACACAT 780
 QY 2019 TCGAAT-GATGATGCGTATCTATC-TTGAACCTTCTATATGAGAGAAAG 2071
 Db 781 TTCATGATTAATGCTATCTACTCTTTGAAACCTTCTATATATGAGAAAG 835
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RESULT 10
 B0772836/c 755 bp mRNA linear EST 26-JUL-2002
 LOCUS
 DEFINITION UI-H-FEO-bdn-c-04-0-UI .s1 NCI CGAP FEO Homo sapiens cDNA clone
 UI-H-FEO-bdn-c-04-0-UI 3', mRNA sequence.
 ACCESSION B0772836
 VERSION B0772836.1 GI:21981312
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 755)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: James Martin
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1. 755

Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /issue_type="Chondrosarcoma Cell line"
 /dev_stage="Adult"
 /lab_host="PH10B (Life Technologies)"
 /note="Vector: pT73-Pac (Pharmacia) with a modified
 polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FEO is
 a cDNA library containing the following tissue(s): a pool
 of 3 chondrosarcoma cell lines (grade 2) The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 CGCTACGGAC. The cell lines was provided by Dr James Martin
 of University of Iowa.
 TAG_TISSUE=human grade 2 chondrosarcoma cell line pool
 TAG_LIB=UI-H-FEO
 TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match

Best Local Similarity 99.3%; Pred. No. 4.3e-164;
 Matches 731; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2630 GTGAGCCAGAGCTGATGAGAGACCTAGCTCTGTTGCTCAGAGTTCAGAGTTA 2689
 Db 754 GTGAGCCAGAGCTGATGAGAGACCTAGCTCT- GTTCTCAGATGTTTCAGAGTAN 696
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QY 2690 TCGAATGAGACAGTTAATGATTTCCGAGAGAAATGATGATTAAGCTATACATTG 2749
DB 695 TCGAATGAGACAGTTAATGATTTCCGAGAGAAATGATGATTAAGCTATACATTG 636
QY 2750 TTCAAATTTGAAACCAAGAGATATGCTCATAGATTTTGGAAATTAACAGATCAAGTA 2809
DB 635 TTCAAATTTGAAACCAAGAGATATGCTCATAGATTTTGGAAATTAACAGATCAAGTA 576
QY 2810 TAATGAAAAAAGAAATGAAAAACCAAGAAATATTCGCAAGATTAACAGATTAACCCAT 2869
DB 575 TAATGAAAAAAGAAATGAAAAACCAAGAAATATTCGCAAGATTAACAGATTAACCCAT 516
QY 2870 CACTAATACTTCTCTTGGCAAAACTGCAAGTGTGCTAGCTGTCTTGGGAAAGATATCC 2929
DB 515 CACTAATACTTCTCTTGGCAAAACTGCAAGTGTGCTAGCTGTCTTGGGAAAGATATCC 456
QY 2930 ATGTAATTGAAAAATGATCATGCTCATATGACCCCAAGATTAACAGATTAACATTG 2989
DB 455 ATGTAATTGAAAAATGATCATGCTCATATGACCCCAAGATTAACAGATTAACATTG 396
QY 2990 TAAGAAAAAACAAGACATGCAAGAAAGTGTGCGGACTATCAATTAATGTAATCA 3049
DB 395 TAAGAAAAAACAAGACATGCAAGAAAGTGTGCGGACTATCAATTAATGTAATCA 336
QY 3050 TCTGCAAAATGTGCGCAAGCTTGGGGAACATGATGTGCAAAAGCTTAAGATTTGCTT 3109
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QY 3170 AAAAGGGGATGAAATTAACCTATCAATTTCCCAATCTGCTATGAGATGCTGTTAT 3229
DB 215 AAAAGGGGATGAAATTAACCTATCAATTTCCCAATCTGCTATGAGATGCTGTTAT 156
QY 3230 TTAGTATGAGATTAAGCACTTATGTAAGATTTCTTTAAATATACTATCAGTTAACT 3289
DB 155 TTAGTATGAGATTAAGCACTTATGTAAGATTTCTTTAAATATACTATCAGTTAACT 96
QY 3290 TAATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 3349
DB 95 TAATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 36
QY 3350 TGAATGTTTACTCTG 3365
DB 35 TGAATGTTTACTCTG 20

RESULT 11
BP337464 1035 bp mRNA linear EST 22-NOV-2000
LOCUS 60203515F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183126
DEFINITION 5' mRNA sequence.
ACCESSION BP337464
VERSION BP337464.1 GI:11283715
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1035)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL ac:
<http://image.llnl.gov>
plate: LLM9498 row: n column: 23
High quality sequence start: 5
High quality sequence stop: 695.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4183126"
/issue_type="gliblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1b="NCI CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NciI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match 21.1%; Score 711.6; DB 2; Length 1035;
Best Local Similarity 97.2%; Pred. No. 2.6e-162;
Matches 756; Conservative 0; Mismatches 19; Indels 3; Gaps 3;
QY 1049 AGAATGTGCGACAGAGAGATCCCGAGCCAGAACTCCAGCTCAGGCTTAACAAATG 1108
DB 4 AGAATGTGCGACAGAGAGATCCCGAGCCAGAACTCCAGCTCAGGCTTAACAAATG 63
QY 1109 AGTTGCCAGGCAAGCTTGGAAAGGAATATCATCTCTGCTCCCTTAAGGAGG 1168
DB 64 AGTTGCCAGGCAAGCTTGGAAAGGAATATCATCTCTGCTCCCTTAAGGAGG 123
QY 1169 GAAAAACAGAGGCTGTTTATCATTTGCAAGATCACTTAGCAAGAAAGAAAAAGAT 1228
DB 124 GAAAAACAGAGGCTGTTTATCATTTGCAAGATCACTTAGCAAGAAAGAAAAAGAT 183
QY 1229 CTGAGCTTGAAAAAGTATAGTCTTGTCAATTAAGTACTGCTAGTTGAACGCTTCC 1288
DB 184 CTGAGCTTGAAAAAGTATAGTCTTGTCAATTAAGTACTGCTAGTTGAACGCTTCC 243
QY 1289 GCAAGAGTTCCAACTTTTGAAGAAATGATATGTTATTTGATTAAGTGTGAT 1348
DB 244 GCAAGAGTTCCAACTTTTGAAGAAATGATATGTTATTTGATTAAGTGTGAT 303
QY 1349 CCCAATGAAATATCATTTCCAGAAAGTGTCAAGTCTGTGATTAATTAATCAGTACG 1408
DB 304 CCCAATGAAATATCATTTCCAGAAAGTGTCAAGTCTGTGATTAATTAATCAGTACG 363
QY 1409 CTCGAATCCTGAAAAATCCTCTTAACTTGAAAAATGAGAAGATGCTGTTCAT 1468
DB 364 CTCGAATCCTGAAAAATCCTCTTAACTTGAAAAATGAGAAGATGCTGTTCAT 423
QY 1469 TGTGACATTTTCCCTCATTTATGATGATGAATGTGATCAACCAAGAAAGCATGT 1528
DB 424 TGTGACATTTTCCCTCATTTATGATGATGAATGTGATCAACCAAGAAAGCATGT 483
QY 1529 ATTAATACATCATGAGGCAATTTTGTGATGACAGAGTGAAGAAACAATAGCTCAAGAAG 1588
DB 484 ATTAATACATCATGAGGCAATTTTGTGATGACAGAGTGAAGAAACAATAGCTCAAGAAG 543
QY 1589 AAAACAAACAATGATTTCCCTTCCAGATCTGGAATTAACAGCTTCACTGTGTG 1648
DB 544 AAAACAAACAATGATTTCCCTTCCAGATCTGGAATTAACAGCTTCACTGTGTG 603
QY 1649 GAGGGGCCAGAGCAAGCAAGCAAGCTGAAGAAACATTTAAACTATGTGCCATCTTG 1708
DB 604 GAGGGGCCAGAGCAAGCAAGCAAGCTGAAGAAACATTTAAACTATGTGCCAATC-TG 662
QY 1709 ATGCATTTCTATTAATACTGTAAAGAAACCTTGATCACTGAAGAAACCAATTCAG 1768
DB 663 ATGCATTTCTATTAATACTGTAAAGAAACCTTGATCACTGGAAGAAACCAATTCAG 722
QY 1769 AGCATGCAAGAAATTTGCAATGACATGCAACGAGAGATCATTTAAAGAGAA 1826

Db 723 GGCATGCGAGAG-TTGGCGCTCGCGATGCGACC-GAGAAAGATCCCTTTAAGGAAA 778
|||||
RESULT 12 729 bp mRNA linear EST 23-JAN-2001
LOCUS BF983236
DEFINITION 602305873F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4397083 5',
mRNA sequence.
ACCESSION BF983236
VERSION BF983236.1 GI:12386048
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 729)
REFERENCE NIH_MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10097 row: a column: 20
High quality sequence stop: 665.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4397083"
/issue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-Sport6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 20.4%; Score 687; DB 2; Length 729;
Best Local Similarity 98.9%; Pred. No. 2.5e-156;
Matches 723; Conservative 0; Mismatches 5; Indels 3; Gaps 3;
QY 586 GAGAGGAACTGTTGACATTTGAAGACGAAACCGGATTGCTGTGAGAAACAATGGA 645
DB 1 GAGAGGAACTGTTGACATTTGAAGACGAAACCGGATTGCTGTGAGAAACAATGGA 60
QY 646 AATGAATCAGGTGAAGAGAGCTACTAAAAAGATTGTGAGAAAGAAAATGCTTCTCT 705
DB 61 AATGAATCAGGTGAAGAGAGCTACTAAAAAGATTGTGAGAAAGAAAATGCTTCTCT 120
QY 706 GCATTTCTGATGTTCTTCTGCTCAACAGAAACAATGACTTGTCCAAGATTAAACAGC 765
DB 121 GCATTTCTGATGTTCTTCTGCTCAACAGAAACAATGACTTGTCCAAGATTAAACAGC 180
QY 766 TCTGATTTGCTCAGAAACCAATGACAGATTGAGATTATTCACAAGTTGATGCTCTCA 825
DB 181 TCTGATTTGCTCAGAAACCAATGACAGATTGAGATTATTCACAAGTTGATGCTCTCA 240
QY 826 GTGGAAGAGAACTTTCTTCAACACAGCTCAGCAAAATCTGAGAGAGAGGTCTGGGGC 885
DB 241 GTGGAAGAGAACTTTCTTCAACACAGCTCAGCAAAATCTGAGAGAGAGGTCTGGGGC 300
QY 886 ATGAGAAATACTATCAGATCATCTTTTGAGATTCTTGTGATTTTCAGATCAGAC 945

Db 301 ATGGAATAAATCTCATCAGAAATCATCTTTGAGATTCTTGTGATTTCAGAAATCAGAC 360
QY 946 ACAAGTTTGGCAGAAAGAAAGTGTCAAGCTGCTTAGATGAAGATCTTGAACATAACAGCAAC 1005
DB 361 ACAAGTTTGGCAGAAAGAAAGTGTCAAGCTGCTTAGATGAAGATCTTGAACATAACAGCAAC 420
QY 1006 ATGGGACATGATTTCAAGGCACCATTTGGGAAGTGAATTCAGATGAAGAAATGTGGCAGCAACA 1065
DB 421 ATGGGACATGATTTCAAGGCACCATTTGGGAAGTGAATTCAGATGAAGAAATGTGGCAGCAACA 480
QY 1066 GCATCCCGGAGCCAGAAATCTCAGAGCTCAGGCTTACCAATGGAAGTTGCCAGCCAGCC 1125
DB 481 GCATCCCGGAGCCAGAAATCTCAGAGCTCAGGCTTACCAATGGAAGTTGCCAGCCAG-C 539
QY 1126 TTGGAAGGAGAAATATCATCATCTGCTCCTCTACAGGAGTGAAGAAACAGAGTGGCT 1185
DB 540 TTGGAAGGAGAAATATCATCATCTG-CCTCTACAGGAGTGAAGAAACAGAGTGGCT 598
QY 1186 GTTTACATTTGCCAAGATCATTTAGACAAAGAAAGAAAGATCTGAGCTTGAAAGATT 1245
DB 599 GTTTACATTTGCCAAGATCATTTAGAC-AGAAAGAAAGAAAGATCTGAGCTTGAAAGATT 657
QY 1246 ATAGTTCTTGTCAATTAAGTACTGTGATTGAACAGCTCTTCCGAAAGAGTTCCAAACA 1305
DB 658 ATAGTTCTTGTCAATTAAGTACTGTGATTGAACAGCTCTTCCGAAAGAGTTCCAAACA 717
QY 1306 TTTTGAAGAA 1316
DB 718 TTTTGAAGAA 728

RESULT 13
DR422160 690 bp mRNA linear EST 29-JUN-2005
LOCUS nav08g05.y1 Human pterygium. Unnormalized (nav) Homo sapiens cDNA
DEFINITION clone nav08g05 5', mRNA sequence.
ACCESSION DR422160
VERSION DR422160.1 GI:68324176
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 690)
REFERENCE Wistow, G., Jaworski, C., Aryankalayil, John, M., Rowsey, J. J., Cox, C.,
Reid, T., Dushku, N., and Carper, D.
NEIBank analysis of Human pterygium
Unpublished (2005)
CONTACT: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gwaem@helix.nih.gov
Plate: 08 row: 9 column: 05
Seq primer: universal M13 Reverse.
Location/Qualifiers
1..690
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="nav08g05"
/issue_type="Pterygium"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_1lb="Human pterygium. Unnormalized (nav)"
/note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted
from 9 pooled human pterygia. A directionally cloned cDNA
library in the pCMVSPORT6 vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)

essentially following the protocols of the SuperScript Plasmid System, full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor (5'-pactagttctagatcgacgagggccg(7)15-3'). cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC). Analyzed data available through <http://neibank.nhl.nih.gov>.

ORIGIN

```

Query Match      20.2%; Score 680.4; DB 8; Length 690;
Best Local Similarity 99.1%; Pred. No. 1e-154;
Matches 684; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1854 AACTTATTTGTCAATGATGTCATGTCAGATTTTGGAACTCAACCTTATGAAACAATGGGC 1913
    1 AACTTATTTGTCCCTTATGTCCTCAATGTCAGATTTTGGAACTCAACCTTATGAAACAATGGGC 60

QY 1914 CATTCAAAATGGAAAAAAGCTGCACAAAAAAGGAAATCGCAAAAGAAAGTGTGTGCAGA 1973
    61 CATTCAAAATGGAAAAAAGCTGCACAAAAAAGGAAATCGCAAAAGAAAGTGTGTGCAGA 120

QY 1974 ACATTGAGGAAGTACATAGAGCCCTACAAATTTAATGACACATTGCAATGATAGATGC 2033
    121 ACATTGAGGAAGTACATAGAGCCCTACAAATTTAATGACACATTGCAATGATAGATGC 180

QY 2034 GTATACTCATCTTGAACCTTCTATATATGAAGAAAGATTAAGAAAGTTTGCACTATAGA 2093
    181 GTATACTCATCTTGAACCTTCTATATATGAAGAAAGATTAAGAAAGTTTGCACTATAGA 240

QY 2094 AGATGATAGTGAAGAGGTGATGATGATGATTTGATGATGATGATGATGATGATGATGATG 2153
    241 AGATGATAGTGAAGAGGTGATGATGATGATTTGATGATGATGATGATGATGATGATGATG 300

QY 2154 TTTAAAGAAACCTTTGAACTGATGAAACAGATAGATTTCTCATGCTTTATTTTGA 2213
    301 TTTAAAGAAACCTTTGAACTGATGAAACAGATAGATTTCTCATGCTTTATTTTGA 360

QY 2214 AAAACAATAAATTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAAAGCTGAC 2273
    361 AAAACAATAAATTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATGAAAAAGCTGAC 420

QY 2274 CAAATTAAGAAATACATATATGAGCAATTTACTAGAGCTGAGGAATCCAGACAGAGGAAT 2333
    421 CAAATTAAGAAATACATATATGAGCAATTTACTAGAGCTGAGGAATCCAGACAGAGGAAT 480

QY 2334 AATCTTTACAAAAACAGACAGAGTGCATATGCGCTTTCCAGTGGATTACTGAAAAATGA 2393
    481 AATCTTTACAAAAACAGACAGAGTGCATATGCGCTTTCCAGTGGATTACTGAAAAATGA 540

QY 2394 AAAATTTGCTGAGTAGAGTCAAAAGCCCAATCTTGATTTGAGCTGACACAGCAGTGA 2453
    541 AAAATTTGCTGAGTAGAGTCAAAAGCCCAATCTTGATTTGAGCTGACACAGCAGTGA 600

QY 2454 GTTCAAAACCATGACACAGAAATGAACAAAAGAGTCATTAGTAATTTGCGACTGGA 2513
    601 GTTCAAAACCATGACACAGAAATGAACAAAAGAGTCATTAGTAATTTGCGACTGGA 660

QY 2514 AATCAATCTGCTATGCTACACAGATGGC 2543
    661 AATCAATCTGCTATGCTACACAGATGGC 690

Db 661 AATCAATCTGCTATGCTACACAGATGGC 690

RESULT 14
CA423868/c 701 bp mRNA linear EST 07-NOV-2002
LOCUS DE1N1T0N CA423868.1 GI:24786594
DEFINITION UI-H-FBI-bcd-1-21-0-UI-51 NCI CGAP FBI Homo sapiens cDNA clone
VERSION CA423868
ACCESSION CA423868.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

1 (bases 1 to 701)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail@nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, Dento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..701
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FBI-bcd-1-21-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FBI"
/note="Organ: Chondrosarcoma; Vector: pT73-Pac (pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FBI is a normalized cDNA library derived from a pool of mRNA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCTCGGAC. The cell lines were provided by Dr James Martin from the University of Iowa.
TAG TISSUE=human grade 2 chondrosarcoma cell line pool
TAG LIB=UI-H-FBI
TAG_SEQ=CGTACGAC"

ORIGIN

```

Query Match      19.4%; Score 654.4; DB 6; Length 701;
Best Local Similarity 99.0%; Pred. No. 2.3e-148;
Matches 678; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

QY 2681 CAGAGTTATCGAACATGAGACAGTTAATGATTTCCGAGAGAAATGATGTAAGCTA 2740
    701 CAGAGTTATCGAACATGAGACAGTTAATGATTTCCGAGAGAAATGATGTAAGCTA 642

QY 2741 TACATTGTTCAAAATATGAACACAGAGAGTATGCTCATAGATTTTGAATTCAGA 2800
    641 TACATTGTTCAAAATATGAACACAGAGAGTATGCTCATAGATTTTGAATTCAGA 582

QY 2801 TGCAGAGTATATGAAAAAGAAATGAACCAAGAGAAATTTGCCAGCATTCACA 2860
    581 TGCAGAGTATATGAAAAAGAAATGAACCAAGAGAAATTTGCCAGCATTCACA 522

QY 2861 ATTAACCATCACTAATTAATCTTCTTTGCAAAAACCTGAGTGTGCTAGCCTGTTCTGGG 2920
    521 ATTAACCATCACTAATTAATCTTCTTTGCAAAAACCTGAGTGTGCTAGCCTGTTCTGGG 462

QY 2921 AAGATATCCATGTAATGAGAAATGATCAGCTCATATGACCCCAAGTAATTCAGGAAC 2980
    461 AAGATATCCATGTAATGAGAAATGATCAGCTCATATGACCCCAAGTAATTCAGGAAC 402

Db 461 AAGATATCCATGTAATGAGAAATGATCAGCTCATATGACCCCAAGTAATTCAGGAAC 402

```

Qy	2981	TTTACATTGTGAAGAAAACAAACACATCGCAAAAAGATGTCGCGACTATCAATTAATG	3043
Db	401	TTTACATTGTGAAGAAAACAAACACATCGCAAAAAGATGTCGCGACTATCAATTAATG	342
Qy	3041	GTGAATCATCTGCAAAATGTGGCCAGGCTTGGGGACAATGATGTGCACAAAGCTTAG	3100
Db	341	GTGAATCATCTGCAAAATGTGGCCAGGCTTGGGGACAATGATGTGCACAAAGCTTAG	282
Qy	3101	ATTGGCCTTGCTCAAAATTAAGGAATTTGTAGTGGTTTCAAAAATTAATTCACAAAGA	3160
Db	281	ATTGGCCTTGCTCAAAATTAAGGAATTTGTAGTGGTTTCAAAAATTAATTCACAAAGA	222
Qy	3161	AACATACAAAAGTGGGTAGAAATTAACCTATCAATTCACATTCCTGACTATTCAGAT	3220
Db	221	AACATACAAAAGTGGGTAGAAATTAACCTATCAATTCACATTCCTGACTATTCAGAT	164
Qy	3221	GCTGTTTATTAGTATGATGAGGATTAAGCATTGATTTAAAGATTCTTTAAATTAATCAG	3280
Db	163	GCTGTTTATTAGTATGATGAGGATTAAGCATTGATTTAAAGATTCTTTAAATTAATCAG	105
Qy	3281	TTAAACATTATATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT	3340
Db	104	TTAAACATTATATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT	45
Qy	3341	TCATTAATAATGATTGTTTACTCTG	3365
Db	44	TCATTAATAATGATTGTTTACTCTG	20
RESULT 15			
LOCUS	BG741146	827 bp	mRNA linear EST 15-MAY-2001
DEFINITION	602631817p1_NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776869 5',		
ACCESSION	BG741146		
VERSION	BG741146.1	GI:14051799	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
TITLE	Hominidae; Homo.		
JOURNAL	1 (bases 1 to 827)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgsabbe-remail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: L14M10630 row: b column: 06 High quality sequence stop: 763. Location/Qualifiers 1. 827 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4776869" /lab_host="DH10B (TI phage-resistant)" /clone_lib="NCI_CGAP_Skn3" /note="Organ: skin; Vector: pCMV-SPORT6, Site_1: NotI, Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP library."		
FEATURES			
source			
Query Match	19.4%	Score 652.8	DB 2; Length 827;

Best Local Similarity 96.1%; Pred. NO. 5.8e-148;
Matches 798; Conservative 0; Mismatches 17; Indels 15; Gaps 12;

OY	426	GGGAGGCGCTTGGCGCGCCGCTACATGAACCCGTAGACTACGGACTTGCCCTCTGCATC	485
Db	1	CGGAGGCCCTCTGGCCG-CCGCTACATGMACTCTGAGCTACGGACTTGCCCTCTGCATC	59
OY	486	GTTTGAGAACGCTCATGATGATGATATCTCCACTGCTGAACTCTCTTCCG-CCCACTCTGG	544
Db	60	GTTTGAGAAACGCTCATGATGATGATATCTCCAACTCTGAACTCTCTTCCGCTCCACTCTGG	119
OY	545	TGGAACAAGCTTCTAGTTAGAGACGCTCTGTAATAGTCATGGAAGAGGAACGTGTTGACAA	604
Db	120	TGGAACAAGCTTCTAGTTAGAGACGCTCTGTAATAGTCATGGAAGAGGAACGTGTTGACAA	179
OY	605	TTGGAAGACAGAAACCGGATTTGCTGCTGTCGAGAAAACAATGGAATGAAATCAGGTGTAAAG	664
Db	180	TTGGAAGACAGAAACCGGATTTGCTGCTGTCGAGAAAACAATGGAATGAAATCAGGTGTAAAG	239
OY	665	AGTACTTAAAAAGGATTTGTGCAAGAAAGAAAATGCGTTCTCTGCAATTTCTGAATGTTCTTC	724
Db	240	AGTACTTAAAAAGGATTTGTGCAAGAAAGAAAATGCGTTCTCTGCAATTTCTGAATGTTCTTC	299
OY	725	GTCAACACGGAACAATGAACCTTGTCCAGAGTTAACAGGCTCTGATTTG--CTCGAAG	782
Db	300	GTCAACACGGAACAATGAACCTTGTCCAGAGTTAACAGGCTCTGATTTG--CTCGAAG	359
OY	783	CAATGACAGATTGAGATTTATACAAAGTTGATGCTTCCAGTGGAAAGACAATTTCT	842
Db	360	CAATGACAGATTGAGATTTATACAAAGTTGATGCTTCCAGTGGAAAGACAATTTCT	419
OY	843	TTCAACACAGATTGACGCCAAATCTGGA-GAAGAAGGTCTGGGCGATGGAGAAATACTAT	901
Db	420	TTCAACACAGATTGACGCCAAATCTGGA-GAAGAAGGTCTGGGCGATGGAGAAATACTAT	479
OY	902	CAGAAATCATCTTTGCA-GATTTCTCTGTAATTTAGAAATCAGACAAAGTTTGGCA--G	958
Db	480	CAGAAATCATCTTTGCAAGATTTCTCTGTAATTTAGAAATCAGACAAAGTTTGGCA--G	539
OY	959	AAGGAAGTGTACGCTGCTTTAGATGAAGATCTTGA-CATTAACAGCAATGGGCAGTAT	1017
Db	540	AAGGAAGTGTACGCTGCTTTAGATGAAGATCTTGA-CATTAACAGCAATGGGCAGTAT	599
OY	1018	TCAGGACCATGGAAGTGAATTCAGATGA-AGAAATGTGGCAGCAGAGCATCCCCGGA	1076
Db	600	TCAGGACCATGGAAGTGAATTCAGATGA-AGAAATGTGGCAGCAGAGCATCCCCGGA	659
OY	1077	GCCAGAACTCAGGCTCAGGCTTTCACAAATGG--AAGTTGGCCAGCCAGCCTTGGAGGG	1134
Db	660	GCCAGAACTCAGGCTCAGGCTTTCACAAATGGCAGATTTGCCACGCCAG-CTTGGCAGGG	718
OY	1135	AAGAATATCATCTGCTCTCCCTTACAGAGAGTGGAAAAACCAAGTGGCTGTATTACAT	1199
Db	719	AAGAATATCATCTG-CTCCCTTACAGAGAGTGGAAAAACCAAGTGGCTGTATTACAT	777
OY	1195	-GCCAAGATCATCTTACACAAGAAAAAAGCATCTGAGCTGGAAAAAG	1243
Db	778	AGCCACGGATCACTTAGACAAGAAAGCAATCTGAGCTGGAAACAG	827

Search completed: March 14, 2006, 02:35:01
Job time : 11790 secs

ORIGIN

Query Match

19.4%; Score 652.8; DB 2; Length 827;

US-09-023-655-48

Query Match 38.0%; Score 1278.8; DB 3; Length 1392;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 1311; Conservative 0; Mismatches 77; Indels 5; Gaps 2;

1976 ATTTGAGGAGATGCAATGAGGCGCTTCAAAATTAATGACACATTCGAATGATGATGCGT 2035
 1 ATTTGAGGAGATGCAATGAGGCGCTTCAAAATTAATGACACATTCGAATGATGATGCGT 60
 2036 ATATCATCTTGAACTTTCTATTAATGAGAGAAAGATGAAGAGTTGAGTCATGAG 2095
 61 ATATCATCTTGAACTTTCTATTAATGAGAGAAAGATGAAGAGTTGAGTCATGATGATG 120
 2096 ATGATAGTATGAGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2155
 121 NNN 180
 2156 TAAAGAAACCTTTGAACTTGATGATGAAACAGATGATGATGATGATGATGATGATG 2215
 181 TAAAGAAACCTTTGAACTTGATGATGAAACAGATGATGATGATGATGATGATGATG 240
 2216 ACAAATTAATGTTGAAAGGCTGCTGAAACCCAGAAATGAAATGAAATGAAAGCTGAC 2275
 241 ACAAATTAATGTTGAAAGGCTGCTGAAACCCAGAAATGAAATGAAATGAAAGCTGAC 300
 2276 AATTAAGAAATACCAATATGAGCAATATATAGACTGAGATGAGATGAGATGAGATG 2335
 301 AATTAAGAAATACCAATATGAGCAATATATAGACTGAGATGAGATGAGATGAGATG 360
 2336 TCTTTTCAAAAAACAGACAGAGTGCAATGCGCTTTCCAGTGGATTAATGAAATGAA 2395
 361 TCTTTTCAAAAAACAGACAGAGTGCAATGCGCTTTCCAGTGGATTAATGAAATGAA 420
 2396 AATTTGCTGAAGAGAGTCAAAAGCCACCATCTGATGAGAGTGGACAGAGAGT 2455
 421 AATTTGCTGAAGAGAGTCAAAAGCCACCATCTGATGAGAGTGGACAGAGAGT 480
 2456 TCAAAACCATGACACAGAAATGAAACAAAGAGTCAATGATTAATTTCCACATGAA 2515
 481 TCAAAACCATGACACAGAAATGAAACAAAGAGTCAATGATTAATTTCCACATGAA 540
 2516 TCAATCTGCTTATCGCTACCAAGTGGACAGAGAGTCTGATTAATTAAGAAATGTA 2575
 541 TAAATCTGCTTATCGCTACCAAGTGGACAGAGAGTCTGATTAATTAAGAAATGTA 600
 2576 TTTGTTATCGCTTATCGCTACCAAGTGGACAGAGAGTCTGATTAATTAAGAAATG 2635
 601 TTTGTTATCGCTTATCGCTACCAAGTGGACAGAGAGTCTGATTAATTAAGAAATG 660
 2636 CCAGAGCTGATGAGACACCTACGTCCTGTTGCTCAGAGTGGATTAATGAAATG 2695
 661 CCAGAGCTGATGAGACACCTACGTCCTGTTGCTCAGAGTGGATTAATGAAATG 720
 2696 ATGAGACAGTTAATGATTTCCAGAGAGATGATTAAGAAATGATTAATGATTTGTT 2755
 721 GAGAGACAGTTAATGATTTCCAGAGAGATGATTAAGAAATGATTAATGATTTGTT 780
 2756 ATATGAGACAGAGAGTATGCTCATTAAGTTTGAATTAACATGACAAAGTAAATG 2815
 781 ATATGAGACAGAGAGTATGCTCATTAAGTTTGAATTAACATGACAAAGTAAATG 840
 2816 AAAAGAAATGAAACCAAGAGAAATATTGCCAAGATTAACAAAGTAAATGATTTGTT 2875
 841 AAAAGAAATGAAACCAAGAGAAATATTGCCAAGATTAACAAAGTAAATGATTTGTT 900
 2876 TAACTTTCTTTGCAAAAATGAGAGTGTGCTAGCTTTCTGGGAGAAATATCATGTA 2935
 901 TAACTTTCTTTGCAAAAATGAGAGTGTGCTAGCTTTCTGGGAGAAATATCATGTA 960
 2936 TTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2995
 961 TTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

QY 2996 AAAACAAAGCACTGCAAAAAGAGTGTCCGACTATCAATAATATGATGATGATGATG 3055
 DB 1021 AAAACAAAGCACTGCAAAAAGAGTGTCCGACTATCAATAATATGATGATGATGATG 1080
 QY 3056 AATGAGCAGGCTTGGGGAACAATGATGATGATGATGATGATGATGATGATGATGATG 3115
 DB 1081 AATGAGCAGGCTTGGGGAACAATGATGATGATGATGATGATGATGATGATGATGATG 1140
 QY 3116 AATTAAGAAATTTTGAAGTGTGTTTCAAAATTAATTAACAAAGAAACATTAACAA 3175
 DB 1141 AATTAAGAAATTTTGAAGTGTGTTTCAAAATTAATTAACAAAGAAACATTAACAA 1200
 QY 3176 GGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3235
 DB 1201 GGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1260
 QY 3236 ATGAGATTAAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3295
 DB 1261 ATGAGATTAAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1318
 QY 3296 GATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3352
 DB 1319 TGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1378
 QY 3353 TTGTTTACTCTG 3365
 DB 1379 TTGTTTACTCTG 1391

RESULT 2

US-09-907A-32
 ; Sequence 32, Application US/09907907A
 ; Patent No. 6951923
 ; GENERAL INFORMATION:
 ; APPLICANT: Fisher, Paul B.
 ; APPLICANT: Leszczynska, Magdalena
 ; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESENCE A
 ; FILE REFERENCE: TERMINAL CELL DIFFERENTIATION AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/09/907,907A
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: US 09/243,277
 ; PRIOR FILING DATE: 1999-02-02
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 32
 ; LENGTH: 458
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 342, 355, 365, 368, 375, 381, 385, 414, 445
 ; OTHER INFORMATION: a or c or g or t
 US-09-907A-32

Query Match 11.2%; Score 376.4; DB 3; Length 458;
 Best Local Similarity 97.7%; Pred. No. 6; 6e-91;
 Matches 388; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2969 AATTCAGAACTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3028
 DB 1 AATTCAGAACTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 60
 QY 3029 AATTCAGAACTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3088
 DB 61 AATTCAGAACTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 QY 3089 ACAAAGGCTTGAATTTGCTGCTCAAAATTAAGAAATTTGATGATGATGATGATG 3148
 DB 121 ACAAAGGCTTGAATTTGCTGCTCAAAATTAAGAAATTTGATGATGATGATGATG 180
 QY 3149 ATTCAACAAAGAAACATTAACAAAGGAGTGAATTAATTAATTAATTAATTAATTA 3208

APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yundong
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc-fl_genes Version 2.0
SEQ ID NO 771
LENGTH: 2590
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (190)..(2223)
US-09-799-451-771

Query Match 5.3%; Score 179.6; DB 3; Length 2590;
Best Local Similarity 47.6%; Pred. No. 1,66-37;
Matches 999; Conservative 0; Mismatches 949; Indels 150; Gaps 10;

QY 1048 GAGAAAGTGGACGACAGAGATCCCGAGCCAGAACTCCAGCTCAGGCTTACCAATG 1107
DB 154 GGGACGCTCCCTGGGACAGACTTACTAGAGAGATGAGCTTGGCTTACCAATG 213
QY 1108 GAAATGCCCAAGCAGCTTGGAGGAGATATCATCTCTCTCTACAGGAGT 1167
DB 214 GAGGTATCATGCTCCCTGGAGGAGATATCATCTCTCTCTACAGGAGT 273
QY 1168 GAAAAACGAGAGTGGCTTTCATTTGCCAAGATCCTTACAAAGAAAGAAAGCA 1227
DB 274 GGGAAACCGGAGGCTGCTTATGTGGCCAGCGGACCTAGAGCTGTGTGAGAGC- 332
QY 1228 TCTGAGCTGGAAGATTAAGTCTTGTTCATTAAGTACTGCTAGTGAACAGCTTTC 1287
DB 333 -----CAGGTGTGTATGTGTCAAGGGGTGACCTGTGACCCAGC---AT 378
QY 1288 CGCAGAGATTCACCAATTTTGAAGAAATGATGTGTATTTGATTTAAGTGTAT 1347
DB 379 GGTGAAGAGTTCAAGGCGCATGTGTGATGACGCTGACCGTGACAACTCTAGTGGGAGC 438
QY 1348 ACCCACTGAAAAATATCATTTCCAGAAAGTGTCAATCCTGTGATTTATCAATACA 1407
DB 439 ATGGGACACGTGCTGCTTGGCCACCTGGCCCGGTGATGACCTGTCACTTCACTCA 498
QY 1408 GCTCAATCTTTGAAAACTCCCTTAAACTTGAAGAAATGAGAAATGCTGTGTTCA 1467
DB 499 GCGAGACTTCTGAGATGAGCACTGACGACCCCGA-----GAGAGAGAGCAGTGGAG 552
QY 1468 TTGTCAAGCTTTTCCCTCATTTATCATGTGAATGTCTATCAACCAAGAGAGAGT 1527
DB 553 CTCACGTGTCTTCCCTGATCGTGTGATGATGATGACACACGCAAGAGAGACGCTG 612
QY 1528 TATATTAACATCTGAGGCAATTTTGTATGACAGAGTTGAAAAACAATAGATCAAGAAA 1587
DB 613 TACAAAGTATCATGTAGCCAGTACT-----AGAACTTAACTCCAGAGG 657
QY 1588 GAAAAACAACAGATGATTTCCCTTCCAGATACCTGGAATACAGCTTCACTGATGTT 1647
DB 658 GACCA-----GCCGTAACCCAGAGTCTGTGCTCAAGCTCTCCAGGAGACT 705
QY 1648 GGAGGGGCGACGAGAGCAAGCAAGCTGAAGAACATTTTAAAGTATGTGCAATCTT 1707

DB 706 GGGGGGCTCCAACTGATGGGCGATCAACCAAGCTCTCAGCTCTGTGCAACTTG 765
QY 1708 GATGATTTACTATTAAACCTGTAAAGAAAACCTGTATCACTGAAAAACCAATACAG 1767
DB 766 GACAGTGTGATCATGTCAACCCAGAACTGTGCCCCCACTGAGAGACAGCCAA 825
QY 1768 GAGCCATGCAAGAAATTTGCCATTTGACATGCAACCAAGAAATTCATTTAAAGAAA 1827
DB 826 CAGCTTGGCAACAGTACCACTTGGCCACAGCGGAGCAGAAATCCGTTGGGAGCTTG 885
QY 1828 CTTTGAAGAAATATGACAAAGATTCAACTTATGTCAATAGTCCATGTCA---GAT 1884
DB 886 CTGAAGAACTATGACCAAAATTCATGACCACTGAGATCTGTAGTGGACCGGAAA 945
QY 1885 TTTGAACTCAACCTATGAAATGGGCACTTCAATGGAAGAAAAAAAGCTSCAAAAAA 1944
DB 946 TTTGGAGCAATATGATAGGACAGAGGTGTGAAGCTGATGAGGCTGCTGTGCT 1005
QY 1945 GGAATTCGCAAGAACGTGTTTGTGAGAACATTTGAGGAAGTACATGAGCCCTACAA 2004
DB 1006 GGGCTTCAGAGCAACGGGTGTATGCGCTTCACTGAGCGGCTACAAATGACGCTGCTC 1065
QY 2005 ATTAATGACAAATTCGATATGATATGATGCTATCTGAACTTTCTATAATGA 2064
DB 1066 ATTCATGACACCGTCCGCGCGGTGATGCTTGGCTGCGCTCAGAGATTTCTATCAGG 1125
QY 2065 GAGAAAGATTAAGAAATTTGCACTCATAGAAAGATGATGATGAGGTGTGATGAG 2124
DB 1126 GAGCAGCTCACTAAACCAAGATCTGTGTG----- 1156
QY 2125 TATGTGATGTGATGAAGATGAGATGATTTAAAGAAACCTTGAAACTGATGAACA 2184
DB 1157 -----CC 1158
QY 2185 GATGATTTCTGATGATTTATTTTGAAGAAATGTTGAAGAGCTGCTGA 2244
DB 1159 GAGCGCGGCTCTGCTCTGTGATGACGCGAAGAAATGACCTGCGCACTTGGC---A 1215
QY 2245 AACCCAGATATGAAATGAAAGCTGACCAATTTAAGAAATACATAATGAGCAATAT 2304
DB 1216 ACTCATGCGCCAGAGATTCAAATCTGAGATGTGTGAAABAATCTCTGAAGAGCACTTC 1275
QY 2305 ACTAGAGCTGAGAAATCAGCAGAGAAATATCTTTTCAAAAAACAGACAGATGTAT 2364
DB 1276 AGTAGCTCT---AACAGCCCTGGGGTATCATCTTCAACCCGACCCGCAAGCGCACAC 1332
QY 2365 GCGCTTCCAGATGATTTCTGAAATGAAATTTGCTGAGATGAGATCAAGGCCAC 2424
DB 1333 TCCCTCTGCTCTGCTCCAGAGAGCGAGGCTGTGACATGCTGAGCATTCGGGCTCAG 1392
QY 2425 CATCTGATTTGAGCTGACACAGAGAGTGTCAAAACCATGACACAGAAATGAACAAAA 2484
DB 1393 CTACTGATTTGGGCTGGGAAACAGCAGCCAGACACCAATACCAAGAGGAGACAGCAA 1452
QY 2485 GAAGTCATTAAGTAAATTTGCACTGGAATAATCAATCTGCTTATGCTACCAAGTGGCA 2544
DB 1453 GAAGTATCCAGAAAGTTCCAAAGATGAAACCTGAAACCTTCTGTGGCCAGAGTGGCG 1512
QY 2545 GAAGAGGTCTGATTTAAAGAAATGTAAATTTTATTCCTTTATGCTTCTCTACCAAT 2604
DB 1513 GAGAGGGGCTGACATCCCAATGTCATGTGTGTGTGCTGTATGTGGCTCTTGAACCAAT 1572
QY 2605 GAAATAGCAGTGTCCAGGCGGTGTGAGGCAAGAGCTGATGAGAGCACTACGCTGTG 2664
DB 1573 GAAATCTCATGTGTCCAGGCGAGGCGGTGCGGCGGAGTCAAGATTAACGCTTT 1632
QY 2665 GTTGTCAACAGTGTTCAGAGTATTCGAACATGAGACATTAATGATTTCCAGAGAG 2724
DB 1633 GTAGCAACTGAAGGTGACCGGAGAGCTGAAGCGGAGCTGATCAAGAGCGCTGAGAGG 1692
QY 2725 ATGATGTATTAAGCTATATCATTTGTTCAAAAATGAAACAGAGAGATGTCTCATAG 2784

Db 1693 CTGATGAGCAGCAGGCTGCTGTCGCAAAATGACACAGCCGAGTACCAAGCCAG 1752
Qy 2785 ATTTTGAAATTAACATGATCAAGTATATGAAAAAATGAAATCAACAGGAATATT 2844
Db 1753 ATCCGGGATCTGACACAGCAGCAGCTTGACCAAGCGGGCGCCAGCAGCCGAGGAG 1812
Qy 2845 GCCAAGCATTAACAAGATTAACCATCATTAATTAATTTCTTTGGAAAAATGCACTGTG 2904
Db 1813 AACCGCGGACAGCAGTTCCTCCAGTGAAGCAGTCACTGATCTGATCACTGATGTGT 1872
Qy 2905 CTAGCTGTCTTGGGAAAGATATCCATGATTAATGAAGAAATGCAATCAGCTCAATGACC 2964
Db 1873 GCTGTGGGCAATGACGAGCAGCTGCGGAAGTGAGGAGCACCACATGATGATGAAC 1932
Qy 2965 CCAGATTCAGGAATCTTAATTTGTAAGAGAAAAACAAGCCTGCAAAAGAGTGTCC 3024
Db 1933 CCAACTTCTGCACTACTATATATCTTCAGAGGATCCTGTGATATCAACAAAGTCTTC 1992
Qy 3025 GACTATCAAAATTAATGTAATCATCTGC-----AAATGCGCCAGCTTGGGAAACA 3078
Db 1993 AAGAGCTGAAGCCTGGGGGTCTCATCACTGACAGAACTGTGGGAGGTCTGGGTCTG 2052
Qy 3079 ATGATGTGCAACAAAGCTTGAATTTGCTTGTCTCAAAATTAAGAAATTTGTAGTGG 3136
Db 2053 CAGATGATCTACAAAGTCAAGTGAAGCTGCCAGTCTCAAAAGTCCGAGCATGCTGTGG 2110

RESULT 6
US-08-143-576-6
; Sequence 6, Application US/08143576
; Patent No. 5643761
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Jiang, Hongping
; TITLE OF INVENTION: METHOD FOR GENERATING A SUBTRACTED
; TITLE OF INVENTION: CDNA LIBRARY AND USES OF THE GENERATED LIBRARY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/143,576
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43563/JPM/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-143-576-6

Query Match 3.7%; Score 124.6; DB 2; Length 193;

Best Local Similarity 96.5%; Pred. No. 2.3e-23;
Matches 138; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 3007 CTGCAAAAGAGTGTGCGCATATCAATTAATGTGAATCATCTGCAATGTGGCCAG 3066
Db 1 CTGCAAAAGAGTGTGCGCATAT-AAAATAATGTGAATCATCTGCAATGTGGCCAG 59
Qy 3067 GCTTGGGGAACAATGATGTGCAACAAGGCTTAGATTGCTGTGCTCAAAATAGAAT 3126
Db 60 GCTTGGGGAACAATGATGTGCAACAAGGCTTAGATTGCTGTGCTCAAAATAGAAT 119
Qy 3127 TTTGTAGTGTCTTCAAAATTA 3149
Db 120 TTTGTAGTGTCTTCAAAATATCA 142

RESULT 7
US-09-221-268D-11
; Sequence 11, Application US/09221268D
; Patent No. 6720408
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Jiang, Hongping
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH SPECIFICALLY HYBRIDIZE WITH
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING MDA-7 AND PHARMACEUTICAL COMPOSIT
; FILE REFERENCE: A34534-A-8 (070050.1637)
; CURRENT APPLICATION NUMBER: US/09/221,268D
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 08/316,537
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: 08/143,576
; PRIOR FILING DATE: 1993-10-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 193
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-221-268D-11

Query Match 3.7%; Score 124.6; DB 3; Length 193;
Best Local Similarity 96.5%; Pred. No. 2.3e-23;
Matches 138; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 3007 CTGCAAAAGAGTGTGCGCATATCAATTAATGTGAATCATCTGCAATGTGGCCAG 3066
Db 1 CTGCAAAAGAGTGTGCGCATAT-AAAATAATGTGAATCATCTGCAATGTGGCCAG 59
Qy 3067 GCTTGGGGAACAATGATGTGCAACAAGGCTTAGATTGCTGTGCTCAAAATAGAAT 3126
Db 60 GCTTGGGGAACAATGATGTGCAACAAGGCTTAGATTGCTGTGCTCAAAATAGAAT 119
Qy 3127 TTTGTAGTGTCTTCAAAATTA 3149
Db 120 TTTGTAGTGTCTTCAAAATATCA 142

RESULT 8
US-10-131-827-8333
; Sequence 8333, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17284
LENGTH: 12214
TYPE: DNA
ORGANISM: Human
US-09-949-016-17284

Query Match 2.0%; Score 66.6; DB 3; Length 12214;
Best Local Similarity 62.1%; Pred. No. 1e-06;
Matches 105; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1078 CCAGACTCCAGCTCAGGCTTACCAATGGAAGTTCCCGCAGCCTTGGAGGGAAG 1137
DB 11430 CCCAGAAATGAGCTTCGGTCTTACCAATGGAGGTGATCATGCTCCCTGGAGGGCAAG 11489
QY 1138 AATATCATCTGCTCCCTTACAGAGTGGAAAAACAGAGTGGCTTTTACATGGCC 1197
DB 11490 AATATCATCTGCTCCCTTACAGAGTGGAAAAACAGAGTGGCTTTTACATGGCC 11549
QY 1198 AAGATCACTTACAGAAAGAAAGACATCTGAGCTTGAAGTTA 1246
DB 11550 AAGCGCACCTAGAGACTGTGATGAGAGCCAGAGTGTGTATGTGCA 11598

RESULT 11
US-09-590-968B-1
Sequence 1, Application US/09590968B
Patent No. 6737561
GENERAL INFORMATION:
APPLICANT: Ray, Animesh
APPLICANT: Golden, Teresa Ann
TITLE OF INVENTION: GENE ENCODING SHORT INTEGRUMENTS AND USES THEREOF
FILE REFERENCE: 176/60581
CURRENT APPLICATION NUMBER: US/09/590,968B
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,316
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 6184
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-590-968B-1

Query Match 1.9%; Score 63; DB 3; Length 6184;
Best Local Similarity 54.5%; Pred. No. 6.4e-06;
Matches 126; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 2464 ATGACAGAAATGACAAAGAGTCTTAAATTTGCGACTGGAATAATCATCTG 2523
DB 2492 ATGAAATCATCTCAATGAGATACATTTTCCAAATTCGAGATGGCATGTGACATG 2551
QY 2524 CTATTCGTACCAAGTGGCAGAGAGTCTGATATTAAAGATGTAACATTTATTC 2583
DB 2552 TTAGTTGCAAGAGGTTGCTGAGAGAGACTTGAATTAAGCAATGTAACATTTATG 2611
QY 2584 CGTTATGCTCTGTCACCAATGAATAGCATGTGTCAGGCGCGTGTGAGCCGAGCT 2643
DB 2612 CGTTTCGACTTGGCAAGAGCGTGTGCTGATCATTCATCTCTGCGCGGCAAGAAAG 2671
QY 2644 GATGAGAGACCTAGCTCTGTTGCTGCAAGTGTGAGAGTATGAGAA 2694
DB 2672 CCTGATACGACTACATCTCATGTGTTGAGAGAGAAATGTATCTACGCA 2722

RESULT 12
US-09-853-768-10

Sequence 10, Application US/09853768
Patent No. 644446
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION
FILE REFERENCE: RTS-0217
CURRENT APPLICATION NUMBER: US/09/853,768
CURRENT FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 10
LENGTH: 5852
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(4568)
US-09-853-768-10

Query Match 1.8%; Score 62; DB 3; Length 5852;
Best Local Similarity 60.8%; Pred. No. 1.2e-05;
Matches 101; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2477 AACAAAAAGATCTTAAATTTGCACTGGAATAATCAATCTTATCGCTACCA 2536
DB 298 AACAGAGAGTACTTGAATTTGAGCAGACATGAGCAACCTGCTTATGCAACAA 357
QY 2537 CAGTGGCAAGAGTCTGATATTAAAGATGTAACATTTGTTATCGTTATGCTTCG 2596
DB 358 GTATTTGTAAGAGGTGTTGATATACCAAAATGCACTTGTGTGTTGTTGTTGTC 417
QY 2597 TCACCAATGAATAGCATGTGTCAGGCGCGTGTGAGCAGAGC 2642
DB 418 CCACAGATATCATCTATGTTCAATCTTAAAGAGAGCAAGGCG 463

RESULT 13
US-09-853-768-3
Sequence 3, Application US/09853768
Patent No. 644446
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION
FILE REFERENCE: RTS-0217
CURRENT APPLICATION NUMBER: US/09/853,768
CURRENT FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 3
LENGTH: 7037
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (183)...(5957)
US-09-853-768-3

Query Match 1.8%; Score 62; DB 3; Length 7037;
Best Local Similarity 60.8%; Pred. No. 1.3e-05;
Matches 101; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2477 AACAAAAAGATCTTAAATTTGCACTGGAATAATCAATCTTATCGCTACCA 2536
DB 1687 AACAGAGAGTACTTGAATTTGAGCAGACATGAGCAACCTGCTTATGCAACAA 1746
QY 2537 CAGTGGCAAGAGTCTGATATTAAAGATGTAACATTTGTTATCGTTATGCTTCG 2596
DB 1747 GTATTTGTAAGAGGTGTTGATATACCAAAATGCACTTGTGTGTTGTTGTTGTC 1806
QY 2597 TCACCAATGAATAGCATGTGTCAGGCGCGTGTGAGCAGAGC 2642
DB 1807 CCACAGATATCATCTATGTTCAATCTTAAAGAGAGCAAGGCG 1852


```
RESULT 14
US-09-222-575-46/c
; Sequence 46, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-46

Query Match          1.6%; Score 54.6; DB 3; Length 371;
Best Local Similarity 52.7%; Pred. No. 0.00023;
Matches 164; Conservative 0; Mismatches 144; Indels 3; Gaps 2;

QY 2555 TGGATATTAAAGATGTATACATTTGTTATCCGTTATG-GTCTGTCACCAATGAATAGCC 2613
DB 364 TTGACATTGCACAGTGCATCTTGTCACTCTTCATGAGTAATGTGGGCAATGTCTCAAA 305
QY 2614 ATGGTCAGAGCCCGGTGTCAGAGCAGCTGATGAGACCTAGCTGCTGTTGCTCAG 2673
DB 304 ATGATCCAAACAGGCGAGAGAGCAAGAGCAAGCTAGCAAGTCTCTTCTTGACTAGT 245
QY 2674 AGTGGTTCAGAGTTATCGAATGACATGAGACAGTTAATGATTTCCGAGAGAGATGAT 2733
DB 244 AATGCTT--GGTGTATTTGAAAAAGAACAAATTAACATGTACAAAGAAAAATGATGAAT 187
QY 2734 AAAGCTATACATTTGTTCAAAATATGAAACCAAGAGATGCTCATTAAGTTTGGAA 2793
DB 186 GACTTATTTTACGCTTCAGACATGGGCGAAGCAGATTTTGAAGGAAAAAGTTCTGCAT 127
QY 2794 TTACGATGCAAAAGTATATGAAAAAGAAATGAAAAACCAAGAAATATTTGCCAAGCAT 2853
DB 126 ATACGACTCATGAAAAATTCATCAGAGTATGTCAAGAAAAACAAACCTGTACTGAT 67
QY 2854 TACAAGATTA 2864
DB 66 AAGGAAAAATTA 56

RESULT 15
US-09-389-681-46/c
; Sequence 46, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-46
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Query Match          1.6%; Score 54.6; DB 3; Length 371;
Best Local Similarity 52.7%; Pred. No. 0.00023;
Matches 164; Conservative 0; Mismatches 144; Indels 3; Gaps 2;

QY 2555 TGGATATTAAAGATGTATACATTTGTTATCCGTTATG-GTCTGTCACCAATGAATAGCC 2613
DB 364 TTGACATTGCACAGTGCATCTTGTCACTCTTCATGAGTAATGTGGGCAATGTCTCAAA 305
QY 2614 ATGGTCAGAGCCCGGTGTCAGAGCAGCTGATGAGACCTAGCTGCTGTTGCTCAG 2673
DB 304 ATGATCCAAACAGGCGAGAGAGCAAGAGCAAGCTAGCAAGTCTCTTCTTGACTAGT 245
QY 2674 AGTGGTTCAGAGTTATCGAATGACATGAGACAGTTAATGATTTCCGAGAGAGATGAT 2733
DB 244 AATGCTT--GGTGTATTTGAAAAAGAACAAATTAACATGTCAAGAAAAATGATGAAT 187
QY 2734 AAAGCTATACATTTGTTCAAAATATGAAACCAAGAGATGCTCATTAAGTTTGGAA 2793
DB 186 GACTTATTTTACGCTTCAGACATGGGCGAAGCAGATTTTGAAGGAAAAAGTTCTGCAT 127
QY 2794 TTACGATGCAAAAGTATATGAAAAAGAAATGAAAAACCAAGAAATATTTGCCAAGCAT 2853
DB 126 ATACGACTCATGAAAAATTCATCAGAGTATGTCAAGAAAAACAAACCTGTACTGAT 67
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DB 66 AAGGAAAAATTA 56

Search completed: March 12, 2006, 05:35:44
Job time : 1014 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: March 13, 2006, 15:10:59 ; Search time 12661 Seconds
(without alignments)
4601.891 Million cell updates/sec

Title: US-09-515-363c-2

Perfect score: 5311
Sequence: 1 MSGNSTDENFRYLISCFRA.....LPITFPNLYSRCLFSDSD 1025

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5083141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abseq04
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5311	100.0	3380	6	CQ776470 Sequence
2	5311	100.0	3380	6	CS108225 Sequence
3	5311	100.0	3380	6	CS113027 Sequence

4	5311	100.0	3380	8	AF095844	Homo sapi
5	5307	99.9	3434	6	CS033863	Sequence
6	5307	99.9	3434	6	CS036676	Sequence
7	5307	99.9	3434	6	CS042815	Sequence
8	5307	99.9	3434	6	CS045628	Sequence
9	5285	99.5	3372	6	AX300832	Sequence
10	5285	99.5	3373	8	AX300832	Sequence
11	4199	79.1	3078	8	AY075132	Mus muscu
12	4194	79.0	3771	6	CQ777379	Sequence
13	4194	79.0	3771	9	AF374384	Mus muscu
14	4080.5	76.8	3635	9	BC080200	Mus muscu
15	3954	74.4	2540	8	BC078180	Homo sapi
16	3358	63.2	2028	6	CQ729104	Sequence
17	2874	54.1	1776	6	AX714144	Sequence
18	2874	54.1	1776	6	AK056293	Homo sapi
19	2690.5	50.7	2468	6	BC025508	Mus muscu
20	2442	46.0	1443	6	AX300841	Sequence
21	2271.5	42.8	2050	9	BC004031	Mus muscu
22	2072	39.0	1392	6	AR379503	Sequence
23	2021	38.1	1204	8	BC007966	Homo sapi
24	1995	37.6	1284	6	AX300838	Sequence
25	1508	28.4	3458	6	BC073528	Xenopus l
26	1357.5	25.6	2493	4	BT020952	Bos tauri
27	1356	25.5	2326	9	AF316999	Mus muscu
28	1356	25.5	2326	9	BC029209	Homo sapi
29	1352	25.5	2584	8	BC014949	Homo sapi
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41	1091.5	20.6	4372	6	CS130808	Sequence
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45	1090.5	20.5	3065	6	CS113026	Sequence

ALIGNMENTS

RESULT 1
LOCUS CQ776470 3380 bp DNA
DEFINITION Sequence 156 from Patent EP1394274.
ACCESSION CQ776470
VERSION CQ776470.1 GI:45379860
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
AUTHORS Methods of testing for bronchial asthma or chronic obstructive
TITLE pulmonary disease
JOURNAL Patent: EP 1394274-A 156 03-MAR-2004;
Genex Research, Inc. (JP)
FEATURES
source
1..3380
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 1.77e-312 Length: 3380
Pred. No.: 3380

Score: 5311.00 Matches: 1025
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
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QY 21 ArgValIysMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
DB 229 AGGGTGAATAATGATACATCCAGGTGAGCGCTGCTGACTGACTGACCTTTCGCTGCA 288
QY 41 GluValIlyGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 289 GAGGTGAAAGAGAGATTCCAGAGACAGTCGCCACCTCCGGAAACATGCAGCAGTTGAA 348
QY 61 LeuLeuLeuSerThrLeuGluIlySgIlyValITrPHisLeuGlyITrPThrArgGluPheVal 80
DB 349 CTGCTCTAGACACTTGGAGAAAGGAGTGGCACTTGCTGGACTGGGAAATTCGTG 408
QY 81 GluAlaIleuArgArgThrGlySerProLeuAlaIlaArgTyrMetAsnProGluLeuThr 100
DB 409 GAGGCCCTCCGAGAACCCGCCACCTCTGCGCCGCCGTACATGAACCTTGAGCTCAG 468
QY 101 AsnLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeu 120
DB 469 GACTTCCCTCTCATCTGTTTGAGAACGCTCATGATGAATATCTCCAACTGCTGAACCTC 528
QY 121 LeuGlnProThrIleuValAsnIlySleuLeuValArgAspValIleuAsnIlySleuGlu 140
DB 529 CTTGACCCCACTCGGTGGACAAAGCTTCTAGTTAGACCTCTTGAGTAAGTCATGAG 588
QY 141 GluGluIleuLeuThrIleGluAspArgAsnArgIleAlaAlaIleGluAsnAsnGlyAsn 160
DB 589 GAGGAACTGTTGACATTTGAAAGACAGAAACCGGATTGCTGCTCAGAAACATATGGAAAT 648
QY 161 GluSerGlyValArgGluLeuLeuIlyValIleValGlnIlyGluLeuThrPheSerAla 180
DB 649 GAATCAGGTGTAAAGAGCTAATMAAAAGATTGTGCAGAAAGAAACCTGGTCTCTGCA 708
QY 181 PheLeuAsnValIleuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer 200
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QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220
DB 769 GATTGCTCAGAAAGCAATGACAGATTTGAGAAATTTATCAAAAGTTGATGCTCTCAAGTG 828
QY 221 GluGluGlnIleuLeuSerThrThrValGlnProAsnLeuGluIlySgIlyValITrPGLyMet 240
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DB 889 GAGAAATAACTCATCAGAAATCATCTTTTGAGATTTCTTCTAGTTTCAAGATCAAGACACA 948
QY 261 SerLeuAlaGluIlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
DB 949 AGTTTGGCAGAAAGAAAGTGTCACTGCTTAGATGAAGTCTTGAGACATTAACAGACATG 1008
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QY 301 SerProGluProGluLeuGlnIleuArgProTyrGlnMetGluValAlaGlnProAlaLeu 320
DB 1069 TCCCCGAGACCAAACTCCAGCTCAGGCTTACCAATGGAAGTTGCCAGCCAGCTTGG 1128
QY 321 GluGlyIlyAsnIleIleIleIleCysLeuProThrGlySerGlyIlySThrArgValAlaVal 340

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DB 1189 TACATTGCCAAGATATCATTTAGACAAAGAAAGAAAAAGCATCTGAGCTGGAAAAAGTTATTA 1248
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DB 1249 GTTCTTGTCATTAAGGTACTGCTAGTTGAACAGCTTCCGCAAGAGATTCACCAATTT 1308
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DB 1369 CCAAGAGTTGTCAAGCTCTGTGATATTATTAACAGTCAAGCTCAATCTTGAAAACTCC 1428
QY 421 LeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuIle 440
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QY 441 IleIleAspGluCysHisHisThrAsnIlySgIlyValIleTyrAsnAsnIleMetArgHis 460
DB 1489 ATCATTTGATGAATGTATCATCACACCAAGAAAGCAGTGTATATATTAATCATGAGGCAT 1548
QY 461 TyrLeuMetGlnIlySleuIlyAsnAsnArgLeuIlySleuGluAsnIlySleuProValIlePro 480
DB 1549 TATTTATGCAAGAGTTGAAAAACATATAGCTCAAGAAAGAAACAAACAGATTCCTCC 1608
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DB 1609 CTTCCTCAAGTACTGGGACTTAACAGCTTCACTGGGTGGAGGGCCCAAGCAAGGCC 1668
QY 501 IlySleuAlaGluGlnHisIleIleuIlySleuCysAlaAsnLeuAspAlaPheThrIleIlySthr 520
DB 1669 AAAGCTGAAGAACATTTTAAACATATGTGCCAACTTGATGCAATTTCTATTAAACCT 1728
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QY 541 IleAlaAspAlaThrArgGluAspProPheIlySgIlySleuLeuGlnIleMetThrArg 560
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DB 1909 TGGGCAATTCMAATGGAAGAAAAAGCTGCAAAAAAGAAATGCAAAAGACGTGTTGT 1968
QY 601 AlaGluHisLeuArgIlyTyrArgGlnAlaLeuGlnIleAsnAspThrIleArgMetIle 620
DB 1969 GCAGAACATTTTGAGAAAGTAAATCAATGAGCCCTTCAATAATTAATGACCAATTCGAATGATTA 2028
QY 621 AsnPalITyrThrHisIleuGluIThrPheTyrArgGlnGluIlySleuAspIlySleuPheAlaVal 640
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QY 641 IleGluAspAspSerAspGluGlyIlyAspAspGluITyrCysAspGlyAspGluAspGlu 660
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QY 661 AspAspLeuIlySleuIlySleuIlySleuAspGluIThrAspArgPheLeuMetIThrLeuPhe 680
DB 2149 GATGATTTAAAGAAACCTTTGAAACTGATGAAACAGATGATTCATGACTTATATTT 2208
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RESULT 2
CS108225

LOCUS CS108225 3380 bp DNA linear PAT 22-JUN-2005

DEFINITION Sequence 233 from Patent WO2005051988.
ACCESSION CS108225
VERSION CS108225.1 GI:68147706
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Abbas, A., Bodary, S., Clark, H., Schoenfeld, J., Williams, P.M.,
Wood, W.I. and Wu, T.D.
TITLE Compositions and methods for the treatment of systemic lupus
erythematosus
JOURNAL Patent: WO 2005051988-A 233 09-JUN-2005;
Genentech, Inc. (US)
FEATURES
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1. 3380
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Score: 5311.00 Matches: 1025
Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
Gaps: 0
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Qy 61 LeuIleuSerThrIleuGlnIyIyGlyValATrphIleuGlyTyTrpThrArgGluPheVal 80
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Qy 81 GluAlaIleuArgArgThrGlyIySerProIleuAlaAlaArgTyMetAaenProGluIleuThr 100
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Qy 469 GACTTGCCTCTGCATCTGTTGAAAGCTCAGATGAATATCTCAACTGCTGAACCTC 528
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Qy 141 GluGluIleuIleuThrlIleGluAaenArgAaenArgIleAlaAlaIleGluAaenArgIyAaen 160
Db 589 GAGAACTGTGTGAATATGAAGACAGAAACCGGATGTGCTGCAGAAACAAATGGAAT 648
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VERSION CS113027.1 GI:68224599
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ORGANISM Homo sapiens
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Homnidae; Homo.

REFERENCE
1 Corfe,B. and Chirakkal,H.
AUTHORS Gene screen
TITLE Patent: WO 2005054507-A 45 16-JUN-2005;
JOURNAL University of Sheffield (GB)
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US-09-515-363c-2 (1-1025) x CS113027 (1-3380)

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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE
 AUTHORS Kang,D.C., Gopalakrishnan,R.V., Wu,Q., Jankowsky,E., Pyle,A.M. and Fisher,P.B.
 TITLE mda-5: An interferon-inducible putative RNA helicase with double-stranded RNA-dependent ATPase activity and melanoma growth-suppressive properties
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (2), 637-642 (2002)
 PUBMED 11805321
 REFERENCE
 AUTHORS Kang,D.-C. and Fisher,P.B.
 TITLE Direct Submission
 JOURNAL Submitted (30-SEP-1998) Urology, Columbia University, P&S, 630 W168th, New York, NY 10032, USA
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
REFERENCE
AUTHORS Abbas, A., Clark, H., Ouyang, N., Williams, P. M., Wood, W. I. and Wu, T. D.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 2005019258-A 3369 03-MAR-2005;
Genentech, Inc. (US)
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 Homidae; Homo.
 REFERENCE
 1 Abbae,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
 AUTHORS
 TITL Composition and methods for the treatment of immune related
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REFERENCE
1 Bahr, G., Cocude, C. and Capron, A.
AUTHORS Rhile polypeptides and its fragments and polynucleotides encoding
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JOURNAL Patent: WO 0185955-A 1 15-NOV-2001;
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DEFINITION Homo sapiens RNA helicase-DEAD box protein RH116 mRNA, complete cds.
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VERSION AY017378.1 GI:12621065
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Cocude,C., Truong,M.-J., Billaut-Mulot,O., Delaert,V., Darissec,E., Capron,A., Mouton,Y. and Bahr,G.M.
TITLE A novel cellular RNA helicase, RH116, differentially regulates cell growth, programmed cell death and human immunodeficiency virus type 1 replication
JOURNAL J. Gen. Virol. 84 (12), 3215-3225 (2003)
REFERENCE
AUTHORS Cocude,C., Truong,M.-J., Billaut-Mulot,O., Truong,M.-J., Capron,A. and Bahr,G.M.
TITLE Identification of a new RNA helicase (RH116) regulated by the immunomodulator Murabutide
JOURNAL Unpublished
AUTHORS Cocude,C., Kolesnitchenko,V., Billaut-Mulot,O., Truong,M.-J., Capron,A. and Bahr,G.M.
TITLE Direct Substitution
JOURNAL Submitted (09-JAN-2001) Laboratoire d'Immunologie Moléculaire de l'infection et de l'inflammation, Institut Pasteur de Lille, 1 rue du Professeur Calmette BP 245, Lille 59019, France
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ORIGIN

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Dd		841	GGCAGGGATTTCAGGCACCATGTGGGAAGTATTTCAATGAATAAGTCTCACACAACAAAAGA	:	900
Oy		300	AlaSerProGluProGluLeuGlnLeuArgProGyrGlnMetGluValAlaGlnProAla	:	319
Dd		901	GTAATCCCCGAGCCAGAACTCGACTCGAGGCTTACCMAATGAAATGGCCCAACAGCT	:	960
Oy		320	LeuGluGlyLysAsnIleIleICysLeuProThrglySerGlyLysThrArgValAla	:	339
Dd		961	CTAGATGGGAAGATATATTATTATCTGCCCTCCACGGGAGTAGTGGAACCAAGAGTGACT	:	1020
Oy		340	ValTyrlIeAlalyAhpHisLeuAhpLysLysLysValAserGluProGlyLysVal	:	359
Dd		1021	GTTTACATCACCAAAGATCACTTGTGACAAAGAAAGACGAGCATCTGTAATCCGGAAAGTT	:	1080
Oy		360	IleValIeuValAnLysValIeuIeuValGluGlnIeuPheAcylGlyGlnPheGlnPro	:	379
Dd		1081	ATCGTCTTGTCATATAGGTATGTATTCACAGAACACTTTTCCGAAAGAGTTCAACCCA	:	1140
Oy		380	PheLeuLysLysTrpYrArgValIleGlyLeuSerGlyAhpThrGlnLeuLysIleSer	:	399
Dd		1141	TATTGAAGAANTGSTATCGAATTTATGATTAAAGTGGCGAATCCAGCTGAATAATCA	:	1200
Oy		400	PheProGluValValLysSerCysAhpIleIleIleSerThrAlaGlnIleLeuGluAsn	:	419
Dd		1201	TTTTCCAGAAAGTGTCAAACTTACCATGTATTTATCAGACCTGCTCAATCTTGAAGAAC	:	1260
Oy		420	SerLeuLeuAnLeuGluAnGlnGluAhpAlaGlyValGlnLeuSerAhpPheSerLeu	:	439
Dd		1261	TCCCTCTTAATCTGGAGAGTGGAGACATGACGCTGGCAGCTGTCAAGATCTTCTCTC	:	1320
Oy		440	IleIleIleAhpGluCysHisHistrAnLysGluAlaValTYrAsnAsnIleMetArg	:	459
Dd		1321	ATTATCATGTATGATGAGTGCATCAACCAACAAAGAGCGCATTTAAACAATCATGAGA	:	1380
Oy		460	HistrLeuMetGlnLysLeuLysAhpAsnAsnArgLeuLysLysGluAnLysProValIle	:	479
Dd		1381	CGATTTTGAAGCAGAAAGTCTGGAACATGACCTTCAGAAACAAACCAACCGCCACTT	:	1440
Oy		480	ProLeuProGlnIleLeuGlnLysLeuThrAlaSerProGlyValGlyGlyAlaThrLysGln	:	499
Dd		1441	CCCCGCGCAGATATCTAGACTGACACCTTCACTGGTGTGGAGCAGCCMAAAGCAG	:	1500
Oy		500	AlaLysAlaGluGlnHisIleLeuLysLeuCysAlaAsnLeuAhpAlaPheThrIleLys	:	519
Dd		1501	TCTGAGGCTGAAAAACATATTTAAATATATGTGCCATCTTGATGCTTACCATTTAA	:	1560
Oy		520	ThrValLysGluAnLeuAhpGlnLeuLysAsnGlnIleGlnGluProCysLysLysPhe	:	539
Dd		1561	ACAGTGAAGAGAAATCTTGTCATCTCAACCAACCAATTAAGAAACCATGCAAGAAATTT	:	1620
Oy		540	AlaIleAlaAhpAlaThrArgLysAhpProPheLysGlyLysLeuGlnIleMetThr	:	559
Dd		1621	GTGATTTGTGTGACACACAGAGAAATCATTTAAAGAAACCTTGAATAATTATGGCA	:	1680
Oy		560	ArgIleGlnThrTYrCysGlnMetSerPrometSerAhpPheGlyThrGlnProTYrGlu	:	579
Dd		1681	AGCATTCAGACTTATCTGCCAAAAAGTCAATGTCAATTTTGGAAACCAACATTTATGAG	:	1740
Oy		580	GlnTPRAlaIleGlnMetGlnLysLysAlaAlaLysLysGlyAsnAsnLysGluArgVal	:	599
Dd		1741	CAGTGGGCAATTCAAATGAGAAAAAACTGCTTAAGACGGAATAATCCGAAAGATCGCGCTC	:	1800
Oy		600	CysAlaGlnHisLeuArgLysTrpArgGlnAlaLeuGlnIleAsnAhpThrIleArgMet	:	619
Dd		1801	TGTGAGAGAACTTTGAGGAAGTACACAAAGCCCTTAACAATCAAGACACATCCGAATG	:	1860
Oy		620	IleAhpAlaTYrTHHisIleGluGlnThrPheTYrAsnGlnGluLYrAsnLysLysPheAla	:	639
Dd		1861	ATTGATGCATATAGCCCACTGAGACATTTCTACACTGATGAGAAAGAAAGAAATGTGGCA	:	1920
Oy		640	ValIleGluAhpAhpSerAhpGluGlyLysAhpGluTYrCysAhpGlyAhpGluAhp	:	659

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Qy	660	GIuabApAsenLeuSlySProLeuLysLeuabPGLuThraPargPheLeuMetThrLeu	679	
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Qy	680	PheheGLuabnaenLysbMeLeuLysArgLeuLaladLuabnProGluLyrGLuLuanGLu	699	
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Qy	700	LysLeuThrLysLeuAArgAntThrLlMetGLuGLnTrThraArgThrgLuSLeuA	719	
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Qy	820	ArgGLytrrgalaaargLlaasPGLuSectThrTyraLleuValalahlaserGLySergLys	839	
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Qy	860	CysValaGlnaenMetLysProGLuGLuTyraLahlLyslleLeuGLuLeuGlnMetGln	879	
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LOCUS Sequence 1065 from Patent EP1394274.
DEFINITION CQ777379
ACCESSION CQ777379
VERSION CQ777379.1 GI:45380363
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 1065 03-MAR-2004;
Genex Research, Inc. (JP)
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source location/Qualifiers
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Score: 4194.00 Matches: 817
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Best Local Similarity: 79.6% Mismatches: 132
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RESULT 13
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DEFINITION Mus musculus strain C57BL/6J melanoma differentiation associated
VERSION AF374384
KEYWORDS gene 5-like protein mRNA, complete cde.
SOURCE AF374384.1 GI:20385627
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3771)
AUTHORS Kang,D.-C. and Fisher,P.B.
TITLES Murine homolog of melanoma differentiation associated gene-5 - a
DESH group RNA dependent ATPase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3771)
AUTHORS Kang,D.-C. and Fisher,P.B.
TITLES Direct Submision
JOURNAL Submitted (26-APR-2001) Urology, Columbia University, P & S, 630
West 168th, New York, NY 10032, USA
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LOCUS BC080200
DEFINITION Mus musculus interferon induced with helicase C domain 1, mRNA
ACCESSION BC080200.1 GI:51329783
VERSION 1
KEYWORDS MGC.
SOURCE MGC.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
REFERENCE
1 (bases 1 to 3635)
Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D.,
Altshuler,S.F., Zeeberg,B., Buerck,K.H., Schaefer,C.F., Bhac,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldi,M.F., Cavaletto,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Millaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hultk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Young,A.C., Shvchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.B.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL 2 (bases 1 to 3635)
PUBMED Director MGC Project.
REFERENCES Direct Submission
AUTHORS Submitted (16-AUG-2004) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gathererburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
Akhter,N., Aylee,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

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Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancipop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLINL at: <http://image.llnl.gov>
Series: IRAC Plate: 177 Row: a Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23956207.
Location/Qualifiers

FEATURES

source

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SDED"

CDS

6..8e-238 Length: 3635
Pred. No.: 4080.50 Matches: 800
Score: 84.4% Conservative: 66
Percent Similarity: 78.0% Mismatches: 109
Best Local Similarity: 76.8% Indels: 51
Query Match: 9 Gaps: 3

ORIGIN

Alignment Scores:

US-09-515-363c-2 (1-1025) x BC080200 (1-3635)

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RESULT 15
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 ACCESSION BC078180
 VERSION 1
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Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heide,F., Diatchenko,L., Marsina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywinski,M.I., Skalska,U., Smaltus,D.E., Scherch,A., Schein,J.E., Jones,S.J., and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2540)

Strausberg,R.

Direct Submission

Submitted (19-JUL-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-rc@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)

Gaithersburg, Maryland

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nih.gov

Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Lalic,P., Legaepi,R., Maduro,O.L., Masello,C., Maekeri,B., Mastrian,S.D., McCluskey,J.C., McDowell,J., Pearson,R., Stantirpop,S., Thomas,P.J., Touchman,J.W., Tsougeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRK Plate: 174 Row: p Column: 16

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2786567.

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CDs

FEATURES

source

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Best Local Similarity: 99.5% Mismatches: 1

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XX      Nucleic acid sequences encoding a Melanoma Differentiation Associated
XX      PT Gene useful for cancer cell growth suppression, apoptosis and anti-viral
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XX      Claim 1; Page 16-18; 152pp; English.
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XX      The present invention relates to an isolated nucleic acid encoding a
XX      CC melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5
XX      CC contains a caspase recruitment domain (CARD) and a RNA helicase motif.
XX      CC Mda-5 is a novel interferon (IFN) inducible gene with structural
XX      CC similarities to RNA helicases and CARD motif containing proteins. Mda-5
XX      CC is induced during terminal differentiation in human melanoma cells
XX      CC antileukemic compound mezerein (MEZ). Mda-5 is useful for identifying
XX      CC compounds that may induce its expression. Mda-5 is useful for treating
XX      CC cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma
XX      CC multistage, cervical cancer, breast cancer, colon cancer, prostate
XX      CC cancer, osteosarcoma, chondrosarcoma and especially where the cancer is a
XX      CC cancer of the central nervous system and apoptosis. The Mda-5 promoter
XX      CC exhibits melanocyte tissue specificity and minimises systemic toxicity.
XX      CC The present sequence is human Mda-5 cDNA
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Db      2449 AGTGAAGTCAAACTCAATGACACAGATGAAACAAAAAACAATCTATTAATTTCCGACT 2508
Qy      781 GlyIyleuIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleu 800
Db      2509 GGAATAATCAATCTGCTTATGCTACCAAGTGGCAAGAAAGTCTGATATTTAAAGAA 2568
Qy      801 CysAsnIleValIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenu 820
Db      2569 TGTAACTTTGTATCGTATGCTGCTGACCAATAAATAGCAAGGCTCCAGGCCGT 2628
Qy      821 GlyArgAlaArgAlaArgIleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleu 840

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Db      2629 GGTGAGCCAGAGCTGATGAGACACTAGCTCTGCTGCTTCAACAGTGTTCAGAGATT 2688
Qy      841 IleGluHISGluThrylsAlaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPa 860
Db      2689 ATGAAACATGACAGACTTAATGATTTCCAGAGAGATGATGATTAAGCTATACATTGT 2748
Qy      861 ValIleAsnIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleu 880
Db      2749 GTTCAAAATATGAAACCAAGAGAGTGTCTCAATGATTTTGGAAATTTACAGATGCAAAAGT 2808
Qy      881 IleMetGluIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleuThryls 900
Db      2809 ATATGAGAAAGAAATGAAACCAAGAGAAATTTGCAAGCATTTACAAAGAAATCCCA 2868
Qy      901 SerIleuIleThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGln 920
Db      2869 TCACTATTAATCTTTCTTTGCAAAAACCTGACAGTGTCTGCTGCTGCGGAAAGATATC 2928
Qy      921 HisValIleGluIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleuThryls 940
Db      2929 CATGTAATTTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2988
Qy      941 ValIleGluIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleuThryls 960
Db      2989 GTTAAAGAAACCAACCACTGCAAAAGAGTGTGCGCACTATCAATTAATGATGATGATGAT 3048
Qy      961 IleCysIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGln 980
Db      3049 ATCTGCAAAATGAGCCAGCTGTGGGAAACAGATGATGATGATGATGATGATGATGATGAT 3108
Qy      981 CysIleuIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGln 1000
Db      3109 TGTCTCAAAATTAAGAAATTTTGTAGTGTGTTTCAAAAATATATCAACAAAGAAACATAC 3168
Qy      1001 LysIleIleValIleuenuIyleuThrylsGlnIleuenuIyleuThrylsGlnIleuenu 1020
Db      3169 AAAAAGTGGTGAATTAATCAATTTCCCAATCTTGACATTCAGAAATGCTGTGTA 3228
Qy      1021 PheSerAspGluAsp 1025
Db      3229 TTTAGTATGAGGAT 3243

RESULT 2
ADJ74904
ID ADJ74904 standard; DNA; 3380 BP.
XX
AC ADJ74904;
XX
DT 20-MAY-2004 (first entry)
XX
DE Marker gene SEQ ID NO:156.
XX
KW bronchial asthma; chronic obstructive pulmonary disease;
KM respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KM gene therapy; marker gene; gene; db.
XX
OS Homo sapiens.
XX
PN EP1394274-A2.
XX
PD 03-MAR-2004.
XX
PF 04-AUG-2003; 2003BP-00254857.
XX
PR 06-AUG-2002; 2002BP-00229312.
PR 20-MAR-2003; 2003BP-00077212.
XX
PA (GENO-) GENOX RES INC.
XX
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX
DR WPI; 2004-193155/19.
XX

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PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.

PS Claim 1, SEQ ID NO 156; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (1) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (1) has respiratory
XX CC and antilastematic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.

XX Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

Alignment Scores:

Score: 0 Length: 3380
Percent Similarity: 5311.00 Matches: 1025
Best Local Similarity: 100.0% Conservative: 0
Query Match: 100.0% Mismatch: 0
DB: 12 Gaps: 0

US-09-515-363c-2 (1-1025) x ADJ74904 (1-3380)

QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20
DB 169 ATGTCAATGGGATTCACACAGAGAAATTTCCGATCTCATCTGTCCTCAGGACC 228
QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
DB 229 AGGGTAAATGTACATCCAGGTGAGCCGTGCTGACATCACTGACCTTTGCTCGCA 288
QY 41 GlnValIleGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 289 GAGGTAAAGAGATTCAGAGACAGTCCACCTCCGGGAAACATGACGGCATTGAA 348
QY 61 LeuLeuLeuSerThrLeuGluIleValIleTyrPheGluTyrThrArgGluPheVal 80
DB 349 CTCCTCTGACACCTTGGAGAAAGAGCTGGCACTTGTTGACTCGGAAATTCGTG 408
QY 81 GlnAlaIleuArgArgTyrGlySerProLeuAlaIleArgTyrMetAsnProGluLeuThr 100
DB 409 GAGGCCCTCCGGAGAACCGGACAGCCCTCTGCGCGCTACATGAACTCTGAGCTCAGC 468
QY 101 AspLeuProSerProSerPheGluAsnAlaIleAspGluTyrLeuGluIleLeuAsnLeu 120
DB 469 GACTTGCCCTTCATCTGTTGAGAACGCTCATGATGATATCTCCAACTGCTGAACCTC 528

QY 121 LeuGlnProThrLeuValAspIleLeuLeuValAlaArgAspValLeuAspIleCysMetGlu 140
DB 529 CTTTCAAGCCACCTCTGGTGGACAGCTTCTTGAAGAGCTCTGTGATTAAGTCATGAG 588
QY 141 GlnGluLeuLeuThrIleGluAspArgAsnArgIleAlaAlaGluAsnAsnGlyAsn 160
DB 589 GAGGAACCTTTGACATTTAAGACAGAAACCGGATTGCTGCTGCAGAAAAACAATGGAAT 648
QY 161 GlnSerGlyValArgGluLeuLeuIleValGlnIleGluAsnTyrPheSerAla 180
DB 649 GATCAGGTGTAAGAGAGCTACTTAAAGATTTGTGCAGAAAGAAATCGTTCTCTGCA 708
QY 181 PheLeuAsnValIleuArgIleThrGlyAsnAsnGluLeuValGlnIleuThrGlySer 200
DB 709 TTTCTGAATGTTCTTCTGTAACAGGAAACAAATGAACTTGCCAAAGTTAAACAGCTCT 768
QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlyValAspGlyProGlnVal 220
DB 769 GATTGCTCAAAAGCAATGACAGATTGAAATTTATCAACAGTTGATGCTCTCAAGTG 828
QY 221 GlnGluGlnLeuLeuSerThrThrValGlnProAsnLeuGluIleValIleTyrGlyMet 240
DB 829 GAAAGCAACTTCTTCAACACAGTTCAGCCAAATCTGAGAGAGAGTCTGGGCATG 888
QY 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValIleSerGluSerAspThr 260
DB 889 GGAATATCATCATCAAGAAATCATTTTGGCAGATTTCTTGATGTTTCAAAATCAGCAACA 948
QY 261 SerLeuAlaGlnGlySerValSerCysLeuAspGluSerLeuGlyIleAsnSerAsnMet 280
DB 949 AGTTTGGCAGAAAGAGATGTCAGCTGCTTGAATGAAGCTTGGACATTAACAGCAACATG 1008
QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
DB 1009 GGCAGATATTCAAGCACCATGGAAGTGAATTCAGATGAAGAGAAATGTGCAGCAAGAGCA 1068
QY 301 SerProGluProGluLeuGlnLeuAspProTyrGlnMetGluValAlaGlnProAlaLeu 320
DB 1069 TCCCCGAGACCAAGATCCACAGCTCAGGCTTTCACAAATGGAAGTTGCCAGCGACTTGG 1128
QY 321 GlnGluIleAsnIleIleIleCysLeuProThrGlnSerGlyIleThrArgValAlaVal 340
DB 1129 GAAAGGAAAGATTCATCATCTGCTCCTTACAGGAGTGGAAAAACAGAGTGGCTGTT 1188
QY 341 TyrIleAlaIleAspAspIleAspAspIleValIleValIleSerGluProGlyIleValIle 360
DB 1189 TACATTGCCAAGGATCATCTTAACAGAAAGAAAGAAAGCAATCGAGCTGGAAAAATTATA 1248
QY 361 ValLeuValAsnIleValLeuLeuValGlnGlnLeuPheArgIleGluPheGlnProPhe 380
DB 1249 GTTCTTGTAATTAAGGTACTGCTAGTTGAACAGCTCTTCCGCAAGAGATTCCAAACATTT 1308
QY 381 LeuIleValTyrTyrArgValIleGlyLeuSerGlyAspThrGlnLeuIleIleSerPhe 400
DB 1309 TTGAAGAAATGGATGTGTATGATTAAGTGAATGAGTAAACCACTGAAATATATATTT 1368
QY 401 ProGluValIleValIleSerCysAspIleIleIleSerThrAlaGlnIleLeuGluAsnSer 420
DB 1369 CCAAGAGTGTCAAGTCCGTGATATATTATTAAGTAAAGCTCAAAATCTTGAAAACTCC 1428
QY 421 LeuLeuAsnLeuGluAsnGlyIleValAspAlaGlyValGlnLeuSerAspPheSerLeuIle 440
DB 1429 CTCCTTAACCTTGGAAAAATGAGAAAGTGTGGTTCCTCAATTGTCACACTTTTCCCTCAT 1488
QY 441 IleIleAspGluCysIleIleIleThrAsnIleValIleValIleValIleValIleMetArgHis 460
DB 1489 ATCATTTGATGATGTATATCACACCAACAAAGAGCGTGTATATTAATCATCATGAGGAT 1548
QY 461 TyrLeuMetGlnIleLeuIleAsnAsnArgLeuIleValGlyGluAsnIleProValIlePro 480
DB 1549 TATTTATGAGAAAGTTGAAAAACAAATAGCTCAAGAAAGAAAAACAAACAGATGATCCC 1608
QY 481 LeuProGlnIleLeuGluIleuThrAlaSerProGlyValGlyIleValIleThrIleGlnAla 500

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Db      1609 CTCTCCAGATACATGAGGACATTAAGAGCTTCACTGCTGTTGGAGGGCCAGAGAAAGCC 1668
Qy      501  LysAlaGluGluHisIleLeuLeuLeuCysAlaAsnLeuAspAlaPheThrIleLeuThr 520
Db      1669 AAGCGTGAAGAAACATTTTAAACATATGCGCAATCTTGATGCAATTTACTATTAAACT 1728
Qy      521  ValIleGluAsnLeuAspGluLeuLeuAsnGlnIleGlnGluProCysIleLeuPheAla 540
Db      1729 GTTAAAGAAACCTTGATCACTGAAACCAATACAGAGCCATGCAAGAAAGTTGGCC 1788
Qy      541  IleAlaAspAlaThrArgGluAspProPheIleGluLeuLeuLeuGlnIleMetThrArg 560
Db      1789 ATTGCAGATGCAACGAGAAAGATCCATTTAAAGAGAACTTGTAGAAATTAATGACAAAG 1848
Qy      561  IleGlnThrTyrcysGlnMetSerPromeSerPheGlyThrGlnProTyrgluGln 580
Db      1849 ATTCAAACTTATGTCMAATGAGTCCAAATGTCAGATTTTGAACTCAACCTTATGACAA 1908
Qy      581  TrpAlaIleGlnMetGluLeuLeuAlaAlaIleLeuGlnIleAsnAspThrIleArgValCys 600
Db      1909 TGGGCCATTCMAATGCAAAAGAAAAAGCTGCAGAAAAAGAAATCGCAAGAACTGTTTGT 1968
Qy      601  AlaGluHisLeuArgIleTyrglnGluAlaLeuGlnIleAsnAspThrIleArgMetIle 620
Db      1969 GCAGAAACATTTGAGAAAGTACAAATGAGCCCTCAAAATTAATGACAAATTCGATGATA 2028
Qy      621  AspAlaTyrrThriIleLeuGluThrPheTyraAsnGluGluLeuAspIleLeuPheAlaVal 640
Db      2029 GATGCGTATCTCATCTTGAAACTTCTTATTAAGAAAGAAAGTAAAGATTGACGTC 2088
Qy      641  IleGluAspAspSerAspGluGluGlyIleAspAspGluTyrcysAspGluAspGlu 660
Db      2089 ATGGAAGATATATGTATGAGGCGGTGATGAGTATGATGTGATGAAGATGAG 2148
Qy      661  AspAspLeuLeuTyrsProLeuLeuLeuAspGluThrAspArgPheLeuMetThrLeuPhe 680
Db      2149 GATGATTTTAAAGAACTTTGAAACTGATGAAACAGATGATTTCTCATGACTTTATTT 2208
Qy      681  PheGluAsnAsnLeuMetLeuLeuArgLeuAlaGluAsnProGluTyrgluAsnGluLeu 700
Db      2209 TTTGAAAAACAATATAAATGTTGAAAGGCTGCTGAAAAACCAGATTTGAAAAATGAAAG 2268
Qy      701  LeuThrIleLeuArgAsnThrIleMetGluGlnIleThrArgThrArgGluGluIleAsnArg 720
Db      2269 CTGACCAAAATTAAGAAATACCATATGAGCAAAATATCTAGAGCTGAGAAATGACGCA 2328
Qy      721  GlyIleIlePheThrIleThrArgGlnSerAlaTyraIleLeuSerGlnIleThrGlu 740
Db      2329 GGAATATCTTTTCAAAAAACAGACAGAGTGCATATGCCGTTTCCAGTGCATTAAGCA 2388
Qy      741  AsnGluLeuPheAlaGluValIleGlyValIleAlaHisIleLeuIleGlyAlaGlyHisSer 760
Db      2389 AATGAAAAAATTTGCTGAAAGTAGAGGTCAAAAGCCACCATCTGATTTGAGAGCTGACACAGC 2448
Qy      761  SerGluPheLeuPromeThrGlnAsnGluGlnIleGluValIleSerIlePheAspThr 780
Db      2449 AGTAGAGTTCAAAACCATGACAGAAAGAAACAAAAACAAGCATTAATAATTTCCGACT 2508
Qy      781  GlyIleIleAsnLeuLeuIleAlaThrThrValIleGluGluGluLeuAspIleLeuGlu 800
Db      2509 GGAATAATCAATCTGCTTATCGCTACCAAGTGCAGCAAAAGAGTCTGCAATTTAAAGAA 2568
Qy      801  CysAsnIleValIleArgTyrglyLeuValThrAsnGluIleAlaMetValGlnAlaArg 820
Db      2569 TGTAAACATGTTATCCCTTATGCTCTGTCACCAATAGCAATAGCCATGAGGCCCGCT 2628
Qy      821  GlyArgAlaArgAlaAspGluSerThrThrValLeuValAlaHisSerGlySerGlyVal 840
Db      2629 GGTGAGCCAGAGGTGATGAGAGCACTACGCTCTGCTGCTCAAGGTTCCAGAGTT 2688
Qy      841  IleGluHisGluThrValAsnAspPheArgGluLeuMetMetTyrlValAlaIleHisCys 860

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Db      2689 ATCGAACATGAGCACTTAATGATTTCCAGAGAGATGATATTAAGCTATACATTTGT 2748
Qy      861  ValIleAsnMetLeuSerProGluGluTyraIleHisIleValIleLeuGluLeuGlnMetGlnSer 880
Db      2749 GTTCAAAATTAATGAAACCAAGAGAGTATGCTCATTAATTTTGAATTTACAGATGCAAAAGT 2808
Qy      881  IleMetGluLeuLeuMetLeuThrIleAsnGlnIleAlaIleHisIleTyrlLeuAsnAsnPro 900
Db      2809 ATATGGAAGAAAGAAATGAAACCAAGAGAAATATGCCCAGACATTAACAAGATTAACCA 2868
Qy      901  SerIleuIleThrPheLeuCysIleAsnCysSerValLeuAlaIleCysSerGlyValAspIle 920
Db      2869 TCACATAATACTTTCTTTCGCAAAACCTCAGTGTCTGACCTGTTCTGGGAAAGATATC 2928
Qy      921  HisValIleGluLeuMetHisIleValAsnMetThrProGluPheIleGluLeuTyrlle 940
Db      2929 CATGTAATGAGAAATATGCAATCGCAATATGACCCAGAAATTCAGAGAACTTTACATT 2988
Qy      941  ValArgGluAsnLeuAlaLeuGlnIleLeuLeuTyrcysAlaAspTyrglnIleAsnGlyIle 960
Db      2989 GTTAAGAGAAACCAAGCACTGCAGAAAGAAAGTGTGCCGACTATCAATTAATGTTGAATC 3048
Qy      961  IleCysLeuGlyGlyGlnAlaIleTyrglyThrMetMetValHisIleGlyLeuAspLeuPro 980
Db      3049 ATCTGCAAAATGTGCGCAGGCTTGGGAGAACATATGATGTGCACAAAGCTTAAGATTTGCC 3108
Qy      981  CysLeuLeuIleArgAsnPheValIleValIlePheLeuAsnAsnSerThrIleLeuGlnIle 1000
Db      3109 TGTCTCAAAATTAAGAAATTTTGTATGTGTTTTCAAAATTAATTCACAAAGAAACAATAC 3168
Qy      1001  LysLeuTrpValGluLeuProIleThrPheProAsnLeuAspTyrsGlnCysCysLeu 1020
Db      3169 AAAAGTGGGTAAATTAACCTATCACTATCAATTTCCAACTTGACTATTCAGAAATCTGTGTTA 3228
Qy      1021  PheSerAspGluAsp 1025
Db      3229 TTTAGTATGATGAGAT 3243

RESULT 3
ADRI4404
ID ADRI4404 standard; DNM; 3380 BP.
XX
AC ADRI4404;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human NF-kappaB pathway-associated gene SegID405.
XX
XX NF-kappaB pathway; antiinflammatory; cytosolic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiaesthetic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnereary; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; gene; de; human.
XX
OS Homo sapiens.
XX
PN MO2004065577-A2.
XX
PD 05-AUG-2004.
XX
XX 13-JAN-2004; 2004MO-US000798.

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XX 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Nadler SG, Neubauer MG, Feder JN, Carman J,
 PI MPI; 2004-562168/54.
 DR P-PSDB; ADRI4405.
 XX
 PT New isolated polynucleotides and polypeptides associated with NF-kappa
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappa pathway.
 XX
 PS Claim 1; SEQ ID NO 405; 237pp; English.

XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappa pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virocidic, antiarthritic, antirheumatic,
 CC gastroenteric, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnerrary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappa pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappa regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked alhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral repliation, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, FAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human gene which is
 CC subject to the novel association with the NF-kappa pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 XX Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 3380
 Score: 5311.00 Matches: 1025
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Gaps: 0
 DB: 13

US-09-515-363C-2 (1-1025) x ADRI4404 (1-3380)

QY 1 MetSerAsnGlyIyrSerThrAspGluAnpPheArGlyrLeuIleSerCySpheArGAla 20
 DB 169 ATGTGAAATGGATATTCACAGACGAGAAATTCGCGATCTCATCTGCTTCACAGGACC 228
 QY 21 ArgValIleMetTyrIleGlnValAGluProValIleuAspTyrLeuThrPheLeuProAla 40
 DB 229 AGGGTGAATAATGTCATCCAGGTGAGCCCTGTGTCGACTACCTGACCTTTCTGCGTCA 288
 QY 41 GluValIleGluGlnIleGlnArgThrValAlaThrSerGlyAnpMetGlnAlaValAGlu 60
 DB 289 GAGGTGAAGAGCAGATTCAAGAGCAGTCCGCACTCCGGGAAACAGCAGGCGAGTTGAA 348
 QY 61 LeuLeuLeuSerThrLeuGluIlyValITrPHisLeuGlyTyrTrpThrArgGluPheVal 80
 DB 349 CTGCTGTGAGCACTTGGAGAGGAGGCTGGCACTTGCTGACTCGGAAATTCGTG 408

QY 81 GluAlaLeuArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
 DB 409 GAGGCCCTCCGAGAACCCGACGCCCTCTGGCCGCCGCTTACATGAACCTGAGCTCAGC 468
 QY 101 AspLeuProSerProSerPheGluAnpAlaHisAspGlyTyrLeuGlnLeuLeuAnpLeu 120
 DB 469 GACTTCCTCTTCATCGTTTGAGAACGCTCATGATGAAATATCTCAATGCTCGAACCTC 528
 QY 121 LeuGlnProThrLeuValAspIlyLeuLeuValArgAspValIleuAspIlySerMetGlu 140
 DB 529 CTTACGCCACTCTGTGTGACAAAGCTTCTAGTTAGACAGCTTGGATTAAGTCATGAGAG 588
 QY 141 GluGluLeuLeuThrIleGluAspArgAnpAlaAlaAlaGluLeuAnpGlyAnp 160
 DB 589 GAGGAACGTGTGCAATTGAAAGCAGAAACCGGATTCGTCTGCACAAAAACAATTGAAAT 648
 QY 161 GluSerGlyValArgGluLeuLeuIlyValAGluIlyGluLeuAnpTrpPheSerAla 180
 DB 649 GAATCAGGTGTAGAGAGCTACTTAANAAGATTGTCAAGAAAGAACTGGTCTTGCA 708
 QY 181 PheLeuAsnValIleuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer 200
 DB 709 TTTCTGAATGTTCTTGTCTCAACAGAAACAATGAATCTTCCAAAGATTAAACAGCTCT 768
 QY 201 AspCySerGluSerAsnAlaGluIleGluAnpLeuSerGlnValAspGlyProGlnVal 220
 DB 769 GATTGCTCAGAAAGCAATCAGATGAGAAATTTACAAAGTTATGCTCTCAAGTG 828
 QY 221 GluGluGluLeuLeuSerThrThrValAGlnProAnpLeuGluIlyGlyValITrGlyMet 240
 DB 829 GAAGACACACTTTTTCACACACAGTTCAGCCAAATCTGGAGAGAGAGTCTGGGCGATG 888
 QY 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValIleSerGluSerAspThr 260
 DB 889 GAAATATACATCATCAAAATCATCTTTTGACAGATTCTTGTAAGTTACAGATCAGACACA 948
 QY 261 SerLeuAlaGluGlySerValSerCySleuAspGluSerLeuGlyIlyIleAsnSerAnpMet 280
 DB 949 AGTTTGGCAGAGAAAGTGCAGCTCTTAGAGAAAGCTTGAGACATTAACACAAACATG 1008
 QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAnpValAlaAlaArgAla 300
 DB 1009 GGCAGGATTCAGGACCACTGGAGAGTGAATTCAGATGAAAGAAATGTGCACGAAGGCA 1068
 QY 301 SerProGluProGluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeu 320
 DB 1069 TCCCGGAGCAGCAACTCCAGCTCAGGCTTACCAATGAGAAAGTCCCGCAGCAGCTTG 1128
 QY 321 GluGlyIlyAsnAlaIleIleIleCySleuProThrGlySerGlyIlySerThrArgValAlaVal 340
 DB 1129 GAAGGAGAAAGATTCATCATCTGCTCCCTTACAGGAGAGTGGAAAAACAGAGTGGCTGT 1188
 QY 341 TyrIleAlaIlyAspHisIleuAspIlyIlyValIlyValIleSerGluProGlyIlyValIle 360
 DB 1189 TACATTGCAAGGATCATTTAGACAGAGAAAGAAAGAAAGCAATCTGAGCTTGAAAGTTAT 1248
 QY 361 ValIleuValAsnIlyValIleuLeuValAGluGlnLeuPheArgIlyGluPheGlnProPhe 380
 DB 1249 GTTCTTGTCAATAAGGATCTGATGTGAACAGCTTCCGCAAGAGGTTCCAAACATTT 1308
 QY 381 LeuIlyIlyTrpTyrArgValIleGlyLeuSerGlyAspThrGlnLeuIlyIleSerPhe 400
 DB 1309 TTGAAGAAATGCTATGCTGATTATGATTAAGTGGATACCCAACTGAAAAATATCATTT 1368
 QY 401 ProGluValValIlySerCyAspIleIleIleSerThrAlaGlnIleuGluAnpSer 420
 DB 1369 CCAAGAGTGTCAAGTCTGTGATATTATTAATAGTACAGCTCAAAATCTTGAAGACTCC 1428
 QY 421 LeuLeuAsnLeuGluAnpGlyIlyAspAlaGlyValAGlnLeuSerAspPheSerLeuIle 440
 DB 1429 CTCTTAAACTTGAAGAAATGAGAAAGATGCGGTTCATATGTCAGACTTTTCCCTCAT 1488
 QY 441 IleIleAspGluCyHisHisIleThrAnpIlyValIlyValIlyAsnAnpIleMetArgHis 460


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Db      1489 ATCATGATGATGATCATCACCAACAAAGACGATGATATTAATCATGAGGCAT 1548
Qy      461 TTTLeuMetGlnlyseuysaenaprgleuylusglubenslysp-oval11lepro 480
Db      1549 TATTATGACGAGAGTTGAAAAACAATAGACTCAAGAAAAAACAACAGATTTCC 1608
Qy      481 LeuProGlnlleuenglueuthrAlaSerProGlyValGlyGlyAlaThrlysglnAla 500
Db      1609 CTTCCTCAGATACCTGGAGCTTACAGCTTCCCTGGTGTGGAGGGCCAGAGCAAGCC 1668
Qy      501 LysAlaGlnGlnHisIleleuylsleuCyAlaAsnleuapAlaPheThrIlelystr 520
Db      1669 AAAGCTGAGAACACACTTTTAAAACTATGCGCAATCTTGATCATTTACTATTAAGT 1728
Qy      521 VallysglnubensleupglnleuylsasnGlnlleGlnlupProCylyslvsPheAla 540
Db      1729 GTTAAAGAAAAACCTTATGATCAACTGAAAAACCAATACAGAGCCATGCAAGAGTTGCC 1788
Qy      541 lleAlaAspAlaThrArgGluAspProPheLyseGlnlyseleuenglulIleMetThrArg 560
Db      1789 ATTGCGATGACACCGAGAGAGATCCATTTAAAGAGAACTTCTAGAAATATGACAG 1848
Qy      561 lleGlnThrTyrcysGlnMetSerProMetSerAspPheGlyThrGlnProTyrglnGln 580
Db      1849 ATTCAAACTTATGTCAAATGATGATCCAAATGTCAGATTTGGAACTCAACCTATGACAA 1908
Qy      581 TTPAlaIleGlnMetGlnlyslslyAlaAlaLyseGlyAsnArglysglnAvalCys 600
Db      1909 TGGGCATTCCAATGCAAAAAAAGCTGCMAAAAAAGGAAATGCAAGAAACCTGTTTGT 1968
Qy      601 AlaGlnHisleuArglystrTyraenGlnAlaLeuGlnlleAsnAspThrIleArgMetIle 620
Db      1969 GCAAGACATTTTGAGAGATGACATGAGGCCCTTCAAAATTTATGACACAAATTCAGAGATA 2028
Qy      621 AspAlaTyrrThrsIseuGlnThrPheTyraenGlnGlnlysaAspLysePheAlaVal 640
Db      2029 GATGCGTATATCATCTTGTGAAACTTCTATATGAAAGAAAGATTAAGAGTTTGCACTC 2088
Qy      641 lleGlnAspAspSerAspGlnGlyGlyAspAspGlnTyrcysAspGlyAspGlnAspGln 660
Db      2089 ATTAGAAGATGATGTGATGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATG 2148
Qy      661 AspAspLeuLysePProleuLyseleuAspGlnThrAspArgPheleuMetThrleuPhe 680
Db      2149 GATGATTTTAAAGAAACCTTTGAAACTGGATGAAACAGATTTCTCATGACTTATTTT 2208
Qy      681 PheGlnAsnAsnlyseMetleuylsArgleuAlaGlnAsnProGlnTyrglnAsnGlnlys 700
Db      2209 TTTGAAAAACAATAAATGTTGAAAAAGCTGCTGAAAAACCAAGATATGAAAAATTGAAAG 2268
Qy      701 LeuThrLyseleuArgAsnThrIleMetGlnGlnTyrrThArgThrGlnGlnSerAlaArg 720
Db      2269 CTGACCAAAATTAAAGAAATACATATAGAGCAATATATCTAGAGCTGAGAAATCAGACGA 2328
Qy      721 GlyIleIlePheThrlystrThArgGlnSerAlaTyrrAlaIseuSerGlnTPIIleThrGln 740
Db      2329 GGAATATCTTTTACAAAAACACACAGAGAGCATATGCGCTTCCAGATGATTTACTGAA 2388
Qy      741 AsnGlnLysePheAlaGlnAlaGlyValLyseAlaHisIleleuIleGlyAlaGlyHisSer 760
Db      2389 AATGAAAAAATTCTCTAGAGTACAGAGATCAAGGCCCACTGATTTGGAGCTGACACAGC 2448
Qy      761 SerGlnPheLyseProMetThrGlnAsnGlnGlnlyslslyValIleSerLysePheArgThr 780
Db      2449 AGTGAAGTTCAAAACCATGACACAGAAATGAACAAAAAGAACTATTAGTAAATTTCCACT 2508
Qy      781 GlyLyseIleAsnleuIleAlaThrThrValAlaGlnGlnGlnlyseAspIlelysgln 800
Db      2509 GGAATAATCATATCTGCTATCGCTACACAGTGCAGAAAGAGTCTGGATATTTAAAGAA 2568
Qy      801 CysAsnIleValIleArgTyrglyleuValThrAsnGlnIleAlaMetValGlnAlaArg 820

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Db      2569 TGTAACTTGTATCCGTTATGCTCTCGTACCAATGAATAATGCAATGCTCCAGGCCGT 2628
Qy      821 GlyArgAlaArgAlaAspGlnSerThrTyrrValIleuValAlaHisSerGlySerGlyVal 840
Db      2629 GGTGAGCCAGAGCTATATAGAGACCTTACGTCCTGTTGCTCAGAGTGTCCAGAGATT 2688
Qy      841 lleGlnIleGlnThrValAsnAspPheArgGlnlyseMetMetTyrrlysaIleHisCys 860
Db      2689 ATGAAACATGAGACAGTATATGATTTCCAGAGAAAGATGATGATATTAAGCTATACATTGT 2748
Qy      861 ValGlnAsnMetLyseProGlnGlnTyrrAlaHisIlelyslleuGlnleuGlnMetGlnSer 880
Db      2749 GTTCAAAATATGAAACCAAGAGAGTATGCTCATTAAGATTTGGAAATTTACAGATGCAAAAGT 2808
Qy      881 lleMetGlnlyseMetLyseThrlysaArgAsnIleAlaLyseHisIleTyrrlysaAsnAspPro 900
Db      2809 ATATGAAAGAAATGAAATGAAACCAAGAGAAATATTTGCCAGATTTACAGAAATTAACCA 2868
Qy      901 SerleuIleThrPheleuCylysaAsnCyserValleuAlaCyseSerGlyGlnIle 920
Db      2869 TCACATATTAACCTTCTCTGCAAAAACGACAGTGTCTAGCCTGTTCTGGGGAAGATATC 2928
Qy      921 HisValIleGlnlyseMetHisIleValAsnMetThrProGlnPheLyseGlnleuTyrrIle 940
Db      2929 CATGTATTTGAGAAATGATCATCAGTCATATATGACCCAGAAATTCAGAGAACTTATCAATT 2988
Qy      941 ValArgGlnAsnlysaIleuGlnlyslslyCyAlaAspTyrglnIleAsnGlyGlnIle 960
Db      2989 GTTAAAGAAACCAACACCTGCAAAAGAGTGTGCGACTATCAATAATATGTAATGTAATC 3048
Qy      961 lleCylyseCyseGlyGlnAlaTyrrGlyThrMetMetValHisIlelysglyleuAspLeuPro 980
Db      3049 ATCTGAAATGTGCGCCAGGCTTGGGAGACATATATGTGTCCACAAAGCTTATAGTTGGCT 3108
Qy      981 CysleuLyseIleArgAsnPheValValIlePheLyseAsnAsnSerThrlyslsGlnTyrr 1000
Db      3109 TGTCTCAAAATATGAAGAAATTTTGTAGTGTGTTTCAAAAATATTTCAACAAAGAAATATC 3168
Qy      1001 LyslyseTyrrValGlnleuProIleThrPheProAsnleuAspTyrrSerGlnCyseleu 1020
Db      3169 AAAAATGGGTAGAAATTTACTTATCATATTTCCAAATCTTGACTATTCAGATGCTGTTTA 3228
Qy      1021 PheSerAspGlnAsp 1025
Db      3229 TTTAGTATGATGAGAT 3243

RESULT 4
AEA23691 standard; DNA; 3380 BP.
AEA23691;
AC AEA23691;
XX
XX
XX 11-AUG-2005 (first entry)
XX
XX
XX Human PRO polypeptide DNA SEQ ID NO 233.
DE
XX
XX
XX immune disorder; PRO; Antiinflammatory; Dermatological;
XX Immunosuppressive; Antineumatic; Antiarthritic; Osteopathic;
XX Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant;
XX de; gene.
XX
XX Homo sapiens.
XX
XX WO2005051988-A2.
XX
XX
XX 09-JUN-2005.
XX
XX
XX 02-MAR-2004; 2004WO-US006460.
XX
XX
XX 03-MAR-2003; 2003US-0451884P.
XX
XX
XX (GETH ) GENENTECH INC.
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PI Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
XX
DR WPI: 2005-417958/42.
P-PSDB; AEA23692.
XX
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or
PT psoriasis.
XX
XX
PS Disclosure; SEQ ID NO 233; 966bp; English.
XX
XX
CC The invention relates to an isolated nucleic acid. The polypeptide,
CC compound or composition, and methods are useful for diagnosing and
CC treating an immune related disorder, e.g. systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,
CC spondylarthropathies, systemic sclerosis, idiopathic inflammatory
CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases
CC including bullous skin diseases, erythema multiforme and contact
CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
CC present sequence represents a human PRO polypeptide DNA.
XX
SQ Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3380
Score: 5311.00 Matches: 1025
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query March: 100.0% Indels: 0
DB: 14 Gaps: 0

US-09-515-363c-2 (1-1025) x AEA23691 (1-3380)
QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20
DB 169 ATGTGAAATGGGATTCACACAGAGAAATTCGGATCTCATCTGTCCTTCAAGGCC 228
QY 21 ArgValLysMetCyrTlleglnValGluProValLeuAspTyrLeuThrPheLeuProAla 40
DB 229 AGGGTAAATGTACATCCAGGTGGAGCTGTGCTGACATCACTGACCTTTCGCCGCA 288
QY 41 GluValLysGluGlnTlleglnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 289 GAGGTAAAGGAGCATTCAGAGACAGTCCACCTCCGGAAACATGACGGCATTTGAA 348
QY 61 LeuLeuLeuSerThrLeuGlnLysGlyValTyrPHisLeuGlyTyrThrArgGluPheVal 80
DB 349 CTGCTGCTGACACTTGGAGAAAGGAGCTGGGACCTTGTTGGACTCGGGAATTCGTG 408
QY 81 GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
DB 409 GAGGCCCTCGGAGAACCGGACACCTCTGCGCGCCGCTACATGAACCTTGAGCTCAGC 468
QY 101 AspLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeu 120
DB 469 GACTTGCCCTCTCATCTGTTGAGAACGCTCATGATGAAATATCTCCACTGCTGAACTTC 528
QY 121 LeuGlnProThrLeuValAspLysLeuLeuValArgAspValLeuAspLysCysMetGlu 140
DB 529 CTTCAAGCCCACTCTGGTGGACAAAGCTTCTAGTTAGAGAGCTTTGGATTAAGCATGGAG 588
QY 141 GluGluLeuLeuThrTlleglnAspArgAsnArgTlleaAlaAlaGluAsnAsnGlyAsn 160
DB 589 GAGCAACTGTTGACAAATGGAAGACAGAAACCGGATTCCTGCTGAGAAAAACAATGGAAAT 648
QY 161 GluSerGlyValArgGluLeuLeuLysArgTllevaGlnLysGlnAsnTrpPheSerAla 180
DB 649 GAATTCAGGTGTAAAGAGCTACTAAAGAAAGATGTGTGAGAAAGAAACCTGATTCCTGCA 708
QY 181 PheLeuAsnValLeuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer 200

DB 709 TTTGAAATGTTCTTCGTAACAGAGAAACAATGAATCTTGCAAGATTAAACAGCTCT 768
QY 201 AspCysSerGlySerAsnAlaGlnTlleglnAsnLeuSerGlnValAspGlyProGlnVal 220
DB 769 GATTGCTCAGAAAGCAATGCACAGATGTGAATTTATCAACAGTTGATGCTCTCAAGTG 828
QY 221 GluGlnGlnLeuLeuSerThrThrValGlnProAsnLeuGlnLysGluValTyrGlyMet 240
DB 829 GAAGAGCAACTCTTCAACCAAGTTCAGCCAAATCTGAGAGAGAGGCTCGGGCATG 888
QY 241 GluAsnAsnSerSerGlySerPheAlaAspSerSerValValSerTluserAspThr 260
DB 889 GGAATTAATCTACAGAAATCACTTTTGGAGATTTCTTGATGTTCAAAATCAGACACA 948
QY 261 SerLeuAlaGlnGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
DB 949 AGTTTGCGAAGAGAGATGTCAGCTGCTTGAATGAAGCTTGGACATTAACAGCAACAG 1008
QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
DB 1009 GGCAGATTCACAGCAACCATGGGAAGTATTCAGATGAAGAGAAATGGCAGACAGAGA 1068
QY 301 SerProGluProGluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeu 320
DB 1069 TCCCCGAGACCAGAACTCCAGCTCAGGCTTACCAATGGAAGTTGCCAGCCAGCCTTG 1128
QY 321 GluGlyLysAsnTllegTllecysLeuProThrGlySerGlyLysThrArgValAlaVal 340
DB 1129 GAGGGAGAAATATCTCATCTGCTCCCTTACAGGAGATGGAAAAACAGATGGCTGTT 1188
QY 341 TyrTlleaLysAspHisLeuAspLysLysLysValLysSerGluProGlyLysValTle 360
DB 1189 TACATGCCAAGATCATCTTAGCAAGAGAAAAACATCTGAGCCTGGAAGAAAGTTATA 1248
QY 361 ValLeuValAsnLysValLeuLeuValGlnGlnLeuPheArgLysGluPheGlnProPhe 380
DB 1249 GTTCTTGTAATGAAGTACTGCTGATGTGAACAGCTTTCGCAAGAGATTCACCAATTT 1308
QY 381 LeuLysLysTyrPyrArgValTllegLysSerGlyAspThrGlnLeuLysTleSerPhe 400
DB 1309 TTGAAGAAATGTGATCTGTTATTTGATTAAGTGTGATACCACTGAAAAATATCATTT 1368
QY 401 ProGluValValLysSerCysAspTllegTllecSerThrAlaGlnTllegGluAsnSer 420
DB 1369 CCAAGAGTTGTCAAGCTCTGTGATATTATTCAGTACAGCTCAATCTTGAAATCTCC 1428
QY 421 LeuLeuAsnLeuGlnAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuTle 440
DB 1429 CTCTTAACCTTGAAAAATGAGAGAAAGTCTGTGTTCATTTGACACTTTCCTCATTT 1488
QY 441 TleTleAspGlnCysHisTlserThrAsnLysGluAlaValTyrAsnAsnTleMetArgHis 460
DB 1489 ATCATTTGATGATGTATCATCACACCAACAAAGACGTGTATTAATATCATCAGAGCAT 1548
QY 461 TyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysLysGluAsnLysAspProValTlePro 480
DB 1549 TATTTATGAGAAAGTTGAAAAACAATAGCTCAAGAAAGAAAAACAACAGATGATCCC 1608
QY 481 LeuProGlnTllegGlnLysLeuThrAlaSerProGlyValGlyGlyValThrLysGlnAla 500
DB 1609 CTTCTCAGATACCTGGAGCTTAACAGCTTCACTGGTGTGGAGGGCCACGAAAGAGCC 1668
QY 501 LysAlaGlnGlnHisTlserLysLeuCysAlaAsnLeuAspAlaPheThrTlleyThr 520
DB 1669 AAGCTGAAGAACACATTTTAAACTATGTGCCAATCTTGATGCAATTTACTATTAACCT 1728
QY 521 ValLysGluAsnLeuAspGlnLeuLysAsnGlnTllegGlnLysProCysLysLysPheAla 540
DB 1729 GTTAAAGAAACCTTATATCACTGAAGAAACAAAATACAGAGCCATGCAAGAGTTGCC 1788
QY 541 TleAlaAspAlaThrArgLysAspProPheLysGlnLysLeuLeuGlnTlleyMetThrArg 560

Db 1789 ATTGACAGATGCAACAGAGAGATCCATTTAAAGAGAACTCTAGAAATATATGACAGG 1848
 Qy 561 TLeGlnThrTyrCysGlnMetSerPrometSerAspPheGlyThrGlnProTyrGlnGln 580
 Db 1849 ATTCAAACTTATATGCAATGAGTCCAGATGTCAGATTTTGAACTCAACCTTATGACAA 1908
 Qy 581 TTPAlaTLeGlnMetGluTyrValAlaTyrLeuGlyAsnArgLysGluArgValCys 600
 Db 1909 TGGGCCATTCGAATGGAAGAAAAAGCTGCAAAAAAGGAATGCAAGAACGCTTTGT 1968
 Qy 601 AlaGlnHisLeuArgLysTyrAsnGluAlaLeuGlnTLeuAsnProThrTLeuGlnTLe 620
 Db 1969 GCAGAACATTTGGAGAGTACCAATGAGGCCCTTCAATTAATGACCAATTTCAATGATA 2028
 Qy 621 AspAlaTyrThrHisLeuGluTyrPheTyrAsnGluGluTyrAsnProTyrPheAlaVal 640
 Db 2029 GATGCGTATATCTATCTTGAACTTCTTATATGAGAGAAAGATTAAGAAATTGCGAGTC 2088
 Qy 641 TLeGluAspAspSerAspGluGlyAspAspGluTyrCysAspGlyAspGluAspGlu 660
 Db 2089 ATAGAAAGATGATGATGATGAGGCTGGTGGATGATGATGATGATGATGATGATGATG 2148
 Qy 661 AspAspLeuTyrAspProLeuTyrLeuAspGluTyrThrAspArgPheLeuMetThrLeuPhe 680
 Db 2149 GATGATTTAAAGAAACCTTGAACCTGATGAACAGATGATGATGATGATGATGATGAT 2208
 Qy 681 PheGluAsnAsnTyrMetLeuTyrAspGluAlaGluAsnProGluTyrGluAsnGluTyr 700
 Db 2209 TTTGAAACCAATTAATATGTTGAAAGAGCTGGCTGTAAGAACCAAAATATGAAATGAAAG 2268
 Qy 701 LeuThrTyrLeuArgAsnThrTLeuMetGluGlnTyrThrArgThrGluGlnGlnSerAlaArg 720
 Db 2269 CTGACCAATTAAGAAATACCAATATGAGCAATATATCTGAGCTGAGAAATGACAGCA 2328
 Qy 721 GlyTLeIlePheThrTyrThrArgGlnSerAlaTyrAlaLeuSerGlnTyrPheGlnTyr 740
 Db 2329 GGAATATATCTTTCAAAACACAGACAGAGCTATGCGCTTCCAGTGAATTTACTGAA 2388
 Qy 741 AsnGluTyrPheAlaGluValGlyValTyrAlaHisHisLeuTLeGlyAlaGlyHisSer 760
 Db 2389 AATGAAATATTTGCTGAGAGAGAGTCMAAGCCACCTGATGATGAGCTGACACAGC 2448
 Qy 761 SerGluPheLysProMetThrGlnAsnGluGlnTyrLeuGluValTLeuSerLysPheArgThr 780
 Db 2449 AGTGAATTCAAACCCATGACACAGATGAAACAAAGAAAGTCAATTAGTAATTTCCGACT 2508
 Qy 781 GlyLysTLeuAsnLeuTLeuAlaThrThrValAlaGluGlnTyrLeuAspTLeuGlu 800
 Db 2509 GGAATAATCAATCTGCTTATCGCTACCAAGTGGCAGAAAGATCTGATATTTAAAGAA 2568
 Qy 801 CysAsnTLeuValTLeuArgTyrGlyLeuValTThrAsnGluTLeuAlaMetValGlnAlaArg 820
 Db 2569 TGTAACTATGTTATCGCTTATGCTCTGTCACCAATGAATTAACATGTCGAGGCCGT 2628
 Qy 821 GlyArgAlaArgAlaAspGluSerThrTyrValTLeuValAlaHisSerGlySerGlyVal 840
 Db 2629 GGTGCGAGCCAGAGCTATGAGACACCTAGCTCTGCTGCTCACTGCTTACAGAGATT 2688
 Qy 841 TLeGluHisGluThrValAsnAspPheArgTyrGlyLysMetTyrLysAlaTLeuHisCys 860
 Db 2689 ATCGAACATGACAGATTAATGATTTCCGAGAGAAAGTATGATTAAGCTATATACATTGT 2748
 Qy 861 ValGluAsnMetLysProGluGluTyrTyrAlaHisLysTLeuGlnTLeuGlnMetGlnSer 880
 Db 2749 GTTCAAAATATGAAACACAGAGAGTATGCTCAATTAAGATTTTGAATTTACGATGCAAAAGT 2808
 Qy 881 TLeuMetGluTyrLysMetLysThrTyrAspAsnTLeuAlaTyrHisTyrLysAsnAsnPro 900
 Db 2809 ATATATGAAAGAAAGAAATGAAACCAAGAGAAATTTTCCAGACATTTACAGAAATTAACCA 2868
 Qy 901 SerLeuTLeuThrPheLeuTyrLysAsnTyrSerValTLeuAlaCysSerGlyGluAspTLe 920
 Db 2869 TCACATAATACTTTCTTTGCAAAACCTGACAGTGTCTAGCTGTCTGGGAAAGATATTC 2928

Qy 921 HisValTLeGluTyrMetHisHisValAsnMetThrProGluPheLysGluLeuTyrTLe 940
 Db 2929 CATGTAAATGAGAAATATGATACATGCTCAATATGACCCAGAAATTCAGAGAACTTACATT 2988
 Qy 941 ValArgGluAsnTyrAlaLeuGlnTyrLysCysAlaAspTyrGlnTLeuGlnTLeu 960
 Db 2989 GTTAAGAGAAACCAAAACCTGCAAAAGAGTGTGCGACTATCAATTAATGATGTAATTC 3048
 Qy 961 TLeCysLysCysGluTyrGlnAlaTyrPheTyrMetMetValHisLysGlyLeuAspLeuPro 980
 Db 3049 ATCTGCAAAATGTGCGCCAGCTTGGGAGACAAATGATGTGCAAAAGCTTATGATTTGCC 3108
 Qy 981 CysLeuTyrTLeuArgAsnPheValValTLeuPheLysAsnAsnSerThrTyrLysGlnTyr 1000
 Db 3109 TGTCTCAAAATTAAGAAATTTTGTAGTGTGTTTCAAAATATATTCACAAAGAAACATTC 3168
 Qy 1001 LysLysTyrValGluLeuProTLeuThrPheProAsnLeuAspTyrSerGluCysGlu 1020
 Db 3169 AAAAGTGGGTAGAAATTAATCACTATCAATTTCCCAATCTTGACTATTCAGATCTGTGTTA 3228
 Qy 1021 PheSerAspGluAsp 1025
 Db 3229 TTTAGTGAATGAGGAT 3243
 Db 3229 TTTAGTGAATGAGGAT 3243
 RESULT 5
 ID AEA36113 standard; DNA: 3380 BP.
 AC AEA36113;
 DT 25-AUG-2005 (first entry)
 DE Human nucleic acid sequence #45.
 KW Screening; gene expression; colorectal tumor; colitis; Crohns disease;
 KW Irritable bowel syndrome; gastrointestinal disease; cytostatic;
 KW Gastrointestinal-gen.; antiinflammatory; ds.
 OS Homo sapiens.
 PN WO2005054507-A2.
 PD 16-JUN-2005.
 PF 03-DEC-2004; 2004WO-GB005078.
 PR 04-DEC-2003; 2003GB-00028048.
 PA (UYSH-) UNITV SHEFFIELD.
 PI Corfe B, Chirakkal H;
 DR WPI; 2005-435407/44.
 PT Screening for nucleic acid molecules exhibiting altered expression in
 PT cells grown in the presence of butyrate, and detection of the nucleic
 PT acid molecules or the encoded polypeptides in diagnosing colorectal
 PT cancer.
 PS
 PS
 PS
 PS
 PS
 XX
 XX
 CC The invention relates to a method of screening for nucleic acid molecules
 CC that show altered expression in a first cell sample comprising comparing
 CC the gene expression profile of the sample with that of a second reference
 CC sample, where the first sample has been grown in the presence of butyrate
 CC or a related carbon source from which butyrate is directly or indirectly
 CC derived, but the reference sample has not. The invention also relates to
 CC a method of detecting at least one nucleic acid molecule associated with
 CC the initiation and/or progression of colorectal cancer in an animal,
 CC comprising providing a biological sample comprising at least one cell to
 CC be tested, contacting the sample with a ligand (preferably a hybridizing
 CC nucleic acid molecule) which binds to at least one nucleic acid and

CC detecting the presence of at least one molecule in the sample, a method
CC of detecting at least one polypeptide associated with the initiation
CC and/or progression of colorectal cancer in an animal comprising providing
CC a biological sample comprising at least one cell to be tested, contacting
CC the sample with at least one ligand that specifically binds at least one
CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
CC an amino acid sequence which varies by the addition, deletion or
CC substitution of at least one amino acid residue and detecting the
CC presence of the polypeptide in the sample, a method of screening for
CC agents that modulate the activity of at least one polypeptide encoded by
CC a gene associated with the initiation and/or progression of colorectal
CC cancer comprising forming a preparation comprising at least one
CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
CC at least one addition, deletion or substitution and at least one agent to
CC be tested and determining the activity of the agent with respect to
CC activity of the polypeptide, and an antibody or its effective binding
CC portion identified by the method, for use as a pharmaceutical. The
CC methods are useful for screening for nucleic acid molecules that show
CC altered expression in a cell sample, and for detecting a nucleic acid
CC and/or progression of colorectal cancer and are useful for detecting or
CC monitoring colorectal cancer, especially adenocarcinoma. The methods are
CC also useful for screening for agents that modulate the activity of at
CC least one polypeptide encoded by a gene associated with the initiation
CC and/or progression of cancer, where agents identified by the method are
CC useful for treating colorectal cancer. The methods could also be used to
CC detect or monitor other conditions such as colitis, Crohn's disease or
CC irritable bowel syndrome, as a screening tool for fiber consumption, as
CC an assay for colon microflora functionality or for early detection of pre
CC -cancerous growth. This sequence represents a human nucleic acid
CC identified by the screening method of the invention.

XX Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3380
Score: 5311.00 Matches: 1025
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-09-515-363C-2 (1-1025) x AEA36113 (1-3380)

QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20
DB 169 ATGTCAATGGGATTCACACAGACGAGAAATTCGGCTATCTCATCTGCTTCACGGGCC 228
QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
DB 229 AGGGTGAATGTATCATCCAGGTGGAGCTGTGCTGACTACCTGACCTTTGCTGCCGA 288
QY 41 GluValIleGlnGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 289 GAGGTAAAGGAGCATTCAGAGACAGTGCACCTCCGGGAACATGACGACGAGTTGAA 348
QY 61 IleuLeuLeuSerThrLeuGlnIleGlnValIleTyrPheIleuGlyTyrThrArgGluPheVal 80
DB 349 CTCTCTGTACGACCTTTGGAGAGGAGCTGGCACTTGTTGGACTCCGGAAATTCGTG 408
QY 81 GluAlaIleuArgArgThrGlySerProLeuAlaIleArgTyrMetAsnProGluLeuThr 100
DB 409 GAGGCCCTCCGGAGAACCGGACAGCCCTCTGGCCGCCGCTACATGAACCTGAGCTCAG 468
QY 101 AspLeuProSerProSerPheGluAsnAlaIleAspGluTyrIleuGlnIleuLeuAsnLeu 120
DB 469 GACTTGCCCTCTCATCTGTGTGAGAACGCTCATGATGAATATCTCCCAACGCTGAACCTC 528
QY 121 LeuGlnProThrLeuValAspIleLeuLeuValIleArgAspValIleuAspIleCysMetGlu 140
DB 529 CTTTCAGCCCACTCTGGTGGACAAAGCTTCTAGTTAGAACGCTTGGATTAAGTGCATGGAG 588
QY 141 GluGlnIleuLeuThrIleGlnAspArgAsnArgIleAlaIleAlaGluAsnAsnGlyAsn 160

DB 589 GAGGAACCTTTGACATTAAAGCAGAAACCGGATTCGTGCACAAAAACAATGGAAT 648
QY 161 GluSerGlyValArgGluLeuLeuIleValIleGlnIleuAsnTyrPheSerAla 180
DB 649 GAATCAGGTGTAAAGAGCTACTAAAGAGATTGTGCAGAAAGAAATCGTTCTCTGCA 708
QY 181 PheLeuAsnValIleuArgGlnThrGlyAsnAsnGlnIleuValGlnGluLeuThrGlySer 200
DB 709 TTTCTGAATGTTCTTGTGTAACACAGAAACAATGAACCTTGCCMAAGTTAAACAGCTCT 768
QY 201 AspCysSerGlnSerSerAsnIleGlnIleuLeuSerGlnValIleAspGlyProGlnVal 220
DB 769 GATTGCTCAGAAAGCAATGAGATGAGAAATTATACAAAGTTATAGTCTCTCAAGT 828
QY 221 GluGlnGlnIleuLeuSerThrThrValGlnProAsnIleuGlnIleuValIleTyrGlyMet 240
DB 829 GAAGACCAACTTCTTCAACACAGTTCAGCCAAATCTGAGAGAGAGGTCTGGGCATG 888
QY 241 GluAsnAsnSerSerGlnSerSerPheAlaAspSerValIleSerGlnSerAspThr 260
DB 889 GAGAAATTAATCATCAGAAATCATCTTTGCAAGATTCTGTAGTTCCAGATCAGACACA 948
QY 261 SerLeuAlaGlnGlySerValSerCysLeuAspGlnSerLeuGlyIleAsnSerAsnMet 280
DB 949 AGTTTGGCAGAAAGAAAGTGCACCTCTTAGAGAAAGCTTGGACATTAACAGCAACATG 1008
QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspSerGlnGluAsnValAlaAlaArgAla 300
DB 1009 GGCAGTGAATTCAGGACCACTGGAGAAATGATTCAATGAAAGAAATGGCCAGCAAGACA 1068
QY 301 SerProGluProGlnIleuGlnIleuArgProTyrGlnMetGluValIleGlnProAlaLeu 320
DB 1069 TCCCGGAGCCAGAAACTCCACAGCTCAGGCCCTTACCAATAGAAAGTTCCCGACCGACTTG 1128
QY 321 GluGlyIleAsnIleIleIleCysLeuProThrGlySerGlnIleuThrArgValAlaVal 340
DB 1129 GAGGGAAGAAATATCATCTGCTCCCTACAGGAGAGTGAAGAAACCAAGAGGCGCTGT 1188
QY 341 TyrIleAlaIleAspAspIleuAspIleuValIleValIleAspGlnProGlyIleValIle 360
DB 1189 TACATTGCCAAGGATCATCTTAGCAAGAAAGAAAGAAACATCTGACCTGGAAGAAATTA 1248
QY 361 ValIleuValAsnIleValIleuLeuValGlnIleuPheArgIleGluPheGlnProPhe 380
DB 1249 GTTCTTGTCATTAAGGATCTGATGTGAACAGCTCTCCGCAAGAGTTCCAAACCATTT 1308
QY 381 IleuIleuIleTyrTyrArgValIleIleGlyLeuSerGlyAspThrGlnIleuIleIleSerPhe 400
DB 1309 TTGAAGAAATGTATGTGTATTATGATTAAAGTGTATGCCAAGTGAAGAAATATCATTT 1368
QY 401 ProGlnValIleIleSerCysAspIleIleIleSerThrAlaGlnIleuGlnIleuAsnSer 420
DB 1369 CAGAAAGTTGTCAAGTCTCTGTATATTATTAATACAGTCAAAATCCTTGAAATCTCC 1428
QY 421 IleuLeuAsnIleuGlnIleuAsnGlyIleuAspIleGlyValIleGlnIleuSerAspPheSerLeuIle 440
DB 1429 CTCTTAAACTTGAAGAAATGAGAAAGTGGGTGTTCAATTGTCCAGCTTTTCCCTCATTT 1488
QY 441 IleIleAspGluCysIleIleIleThrAsnIleuGlnIleValIleTyrAsnAsnIleMetCArgHis 460
DB 1489 ATCATTTGATGAATGTATCATCACCAACAAAGAGGTGTATATTAATCAATCAATGAGCAT 1548
QY 461 TyrLeuMetGlnIleuIleuIleuIleuAsnAsnArgLeuIleuIleuIleuAsnIlePro 480
DB 1549 TATTTGATGCAAGATTTGAAGAAACATTAAGCTACAGAAAGAAACAAACAGATCTCC 1608
QY 481 LeuProGlnIleuIleuGlyLeuThrAlaSerProGlyValIleGlyIleuIleuIleuVal 500
DB 1609 CTTCTCAAGATTACTGGGAGCTTAACAGCTTCACTGTGTGGAGGGGCCAGAGAAAGCC 1668
QY 501 LysAlaGlnGlnIleuIleIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 520

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Db      1669 AAAGCTGAAGAACACATTTTAAACTATGTCCTGATGCTTGTACTTACTATTAATAACT 1728
Qy      521 VALLVSGIAsnuLeuPrgIleuLYsAenGlnIIGlnGluProCysLYsLYsPheA 540
Db      1729 GTTAAAGAAAACCTTATCAATCAAGTGAAGAAACCAATACAGAGCCATGCAAGAACTTGGCC 1788
Qy      541 ILeAlAspAlaThrArgIuAApproPheLYsGluLYsLeuLeuGluIleMetThrArg 560
Db      1789 ATTGCAGATGCACACGAGAGATCCATTTAAAGAGAACTTCTAGAAATTAAGACAGG 1848
Qy      561 ILeGlnThrTYrCysGlnMetSerPrometSerAspPheGlyThrGlnProTYrGlnGln 580
Db      1849 ATTCAAACTTATGTCATAATGAGTCCAAATGTCAGATTTTGAAGTCAACCTTATGAACA 1908
Qy      581 TTPAlaIIGlnMetGluLYsLYsAlaAlaLYsLYsLYsAsnArgLYsGluArgValCys 600
Db      1909 TGGGCAATTCAAATGGAAGAAAAAGCTCAAAAAAGAAATGCAAGAAACCTGTTGT 1968
Qy      601 AlaGlnHISLeuArgLYsTYrAenGlnAlaLeuGlnIleAsnAspThrIleArgMetIle 620
Db      1969 GCGAACAATTTGAGAGATGCAATGAGCCCTTCAAAATTAATGACACAAATTCGAATGATA 2028
Qy      621 AspAlaTYrThrHISLeuGlnThrPheTYrAenGlnGluLYsAspLYsLYsPheAlaVal 640
Db      2029 GATGCTATATCATCATCTTGAAACTTCTTATTAATGAAGAAAGATTAAGAACTTGCAGTC 2088
Qy      641 ILeGluAspAspSerAspGluGluLYsAspAspGluTYrCysAspGluLYsAspGlu 660
Db      2089 ATAGAAGATGATGATGATGAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 2148
Qy      661 AspAspLeuLYsLYsPheLeuLYsLeuAspGluTYrAspArgPheLeuMetThrLeuPhe 680
Db      2149 GATGATTTAAAGAAACCTTTGAAGACTGATGAAACAGATGATTTCTCATGACTTTATTT 2208
Qy      681 PheGluAsnAsnLYsMetLeuLYsArgLeuAlaGluAsnProGluTYrGluAenGluLYs 700
Db      2209 TTTGAAAACCAATTAATGTTGAAGAGCTGCTGAAGAACCCAGAAATATGAAGAAAG 2268
Qy      701 LeuThrLYsLeuArgAsnThrIleMetGluGlnTYrThrArgThrGluGluSerAlaArg 720
Db      2269 CTGACCAAAATTAAGAAATACCAATATGAGCAATATATCTGAGATGAGCAACGA 2328
Qy      721 GlyIleIlePheThrTYrArgGlnSerAlaTYrAlaLeuSerGlnTYrIleThrGlu 740
Db      2329 GGAATATCTTTTCAAAAACACACACAGAGCTCATATGCGCTTTCCAGTGAATTAAGAA 2388
Qy      741 AsnGluLYsPheAlaGluValGlyValLYsAlaHISLeuIleGlyAlaGlyHISer 760
Db      2389 AATGAAAAATTTCTGAGTAGAGAGTCAAGCCACCATCTGATTTGAGCTGACACAGC 2448
Qy      761 SerGluPheLYsPheMetThrGlnAsnGluGlnLYsGluValIleSerLYsPheArgThr 780
Db      2449 AGTAGAGTTCAAAACCAATGACACAGAAATGAACAAAAGAACTCATTTGTAATTTCCACT 2508
Qy      781 GlyLYsIleAsnLeuLeuIleAlaThrThValAlaGluGluGluLYsAspIleLYsGlu 800
Db      2509 GGAATAATCAATCTGCTTATCGCTACACAGTGCAGAAAGAGTCTGATATTAAGAA 2568
Qy      801 CysAsnIleValIleArgTYrGlyLeuValThAsnGluIleAlaMetValGlnAlaArg 820
Db      2569 TGTACATTTGTTATCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2628
Qy      821 GlyArgAlaArgAlaAspGluSerThrTYrValLeuValAlaHISerGlySerGlyVal 840
Db      2629 GGTGAGCCAGACAGCTAGAGACACCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2688
Qy      841 ILeGlnHISGlnThrValaAsnAspPheArgGluLYsMetMetTYrLYsAlaIleHISer 860
Db      2689 ATGGAACATGACAGATTAATGATTTCCAGAGAAAGATGATGATTAAGTATATACATTTGT 2748
Qy      861 ValGlnAsnMetLYsProGluGluTYrAlaHISLeuLYsLeuGlnLeuGlnMetGlnSer 880
Db      2749 GTTCAAAATATGAAGACAGAGATATGCTCATATGATTTTGAAGATTAAGATGCAAGT 2808

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Qy      881 ILeMetGluLYsLYsMetLYsThrLYsArgAsnIleAlaLYsHISTYrLYsAsnAsnPro 900
Db      2809 ATATATGAAAAGAAATGAAAACCAAGAAATATTTGCCAGATTTACAAAGATTAACCA 2868
Qy      901 SerLeuIleThrPheLeuCysLYsAsnCysSerValLeuAlaCysSerGlyIuAappIle 920
Db      2869 TCATCTATATATCTTCTTTGCAAAAACCTGACAGTGTCTAGCTGCTGCTGCTGCTGCTGCTG 2928
Qy      921 HisValIIGlnLYsMetHISHisValaAsnMetThrProGluPheLYsGluLeuTYrIle 940
Db      2929 CATGTATATGAGAAATATGATCACTGCAATATGACCCAGAAATTCAGAAACTTTACAT 2988
Qy      941 ValArgGluAsnLYsAlaLeuGlnLYsLYsCysAlaAspTYrGlnIleAsnGlyIuIle 960
Db      2989 GTNAGAAAACCAAGCACTGCAAGAAAGTGTGCCGACTATCAATTAATGTTGAATATC 3048
Qy      961 ILeCysLYsCysGlyGlnAlaIleProGlyThrMetMetValHISLYsGlyLeuAspLeuPro 980
Db      3049 ATCTGCAAAATGTGCGCAGCTTGGGGAACAATGATGTGCACAAAGCTTATGATTTGGCT 3108
Qy      981 CysLeuLYsIleArgAsnPheValValValPheLYsAsnAsnSerThrLYsLYsGlnTYr 1000
Db      3109 TGTCTCAAAATATAGAAATTTGTATGTGTGTTTCAAAAATTAATTCACAAAGAAACAATAC 3168
Qy      1001 LYsLYsTrpValGluLeuProIleThrPheProAsnLeuAspTYrSerGluCysLYsLeu 1020
Db      3169 AAAAAGTGGGTAGAAATTAATCACTATCACTATTCCAATCTTGACTATTCAGAAATCTGTTTA 3228
Qy      1021 PheSerAspGluAsp 1025
Db      3229 TTTAGTATGATGAGAT 3243

RESULT 6
ADY17563
ID ADY17563 standard; DNA; 3434 BP.
XX
AC ADY17563;
XX
DT 05-MAY-2005 (first entry)
XX
DE DNA encoding a PRO polypeptide, SEQ ID NO 3369.
XX
XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antineumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiaesthetic;
XX Antiallergic; ds; gene; diagnosis.
XX
OS Homo sapiens.
XX
XX WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004MO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX
PA (GENTH ) GEMENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WJ, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX PT treating an immune related disorder, e.g. systemic lupus erythematosus,
XX PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 1; SEQ ID NO 3369; 158bp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
XX CC polypeptide. The polypeptide, agonist or an antagonist, antibody,

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CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 3434 BP; 1157 A; 673 C; 768 G; 836 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3434
Score:	5307.00	Matches:	1024
Percent Similarity:	100.0%	Conservative:	1
Beet Local Similarity:	99.9%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	14	Gaps:	0

US-09-515-363c-2 (1-1025) x ADY17563 (1-3434)

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QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20
DB 223 ATGTCAATGGGTATTCACACAGAGAAATTCGGCTATCTCATCTGCTTCAGGGCC 282
QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
DB 283 AGGGTAAATATGACATCCAGGTGAGACCTGTCTGACTACCTGACCTTTCGCTGCA 342
QY 41 GluValIleGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 343 GAGGTGAAGAGAGATTTCAGAGACAGTGCACCTCCGGGAAACATGACGACATTGAA 402
QY 61 LeuLeuLeuSerThrIleuGluIlyGlyValTTrpIleuGlyTTrpThrArgGluPheVal 80
DB 403 CTGCTCTGAGCAGCTTGGAGAGGAGTCTGACCTGGTGGACTCGGAAATTCGTG 462
QY 81 GluAlaIleuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
DB 463 GAGGCCCTCGGAGAACCGGCAACCTCTGCGCGCCGCTACATGAACCTGAGCTCAG 522
QY 101 AspLeuProSerProSerPheGluAsnAlaIleAspGluTyrLeuGlnLeuLeuAsnLeu 120
DB 523 GACTTCCTCTCATCTGTTGAGAAAGCTCATGATGAATATCTCCAACTGCTGAACCTC 582
QY 121 LeuGlnProThrIleuValAspIlyLeuLeuValArgAspValIleuAspIlyCysMetGlu 140
DB 583 CTTCACCCCACTGTGGAGCAAGCTTGTAGAGACGCTTGTGATGAATGATCAGAG 642
QY 141 GluGluLeuLeuThrIleGluAspArgAsnArgIleAlaAlaIleGluAsnGlyAsn 160
DB 643 GAGAACTGTGCAATTGAGACAGAAACCGAATTCCTCTGCAAAAACATGGAAT 702
QY 161 GluSerGlyValArgGluLeuLeuIyValGlnIlyGluLeuTTrpPheSerAla 180
DB 703 GAATCAGGTGTAGAGAGCTACTAAAGATGTGTGAGAAAGAAACCTGTTCTCTGCA 762
QY 181 PheLeuAsnValIleuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer 200
DB 763 TTTCTAAATGTTCTTGTCAAAACAGAAACAATGAATTTGTCCAAGGTTAAACAGGCTC 822
QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220
DB 823 GATTCCTCAAAAACATGACAGATTCAGAAATTTATCAACAAGTGAATGCTCTCAAGT 882
QY 221 GluGluGlnLeuLeuSerThrThrValGlnProAsnLeuGluIlyGlyValTTrpGlyMet 240
DB 883 GAAAGCAACCTTCTTCAACACACAGTTCAACCAATTCGAGAAAGAGGCTCTGGGCGATG 942
QY 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValIleSerGluSerAspThr 260
DB 943 GAAATTAATCTCATCAGATCATCTTTTGAGATTTCTTGTAGTTTCAGATACAGACACA 1002
QY 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
DB 1003 AGTTTGGCAGAAAGAAATGTCAAGCTGTTAGATGAAGTCTTGGACATTAACAGCAATG 1062
QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
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DB 1063 GGCAGGATTCAGGACCCATGGAGATGTTACAGATGAAGAAATGTGCAGCAAGACA 1122
QY 301 SerProGluProGluLeuGlnIleuArgProTyrGlnMetGluValAlaGlnProAlaLeu 320
DB 1123 TCCCGGAGACCAAGACTCCAGCTCAGCCTTACCAATGGAACTCCAGCCAGCCTTG 1182
QY 321 GluGlyIlyAsnIleIleIleCysLeuProThrGlySerGlyIlyThrArgValAlaVal 340
DB 1183 GAAAGGAAGATATATCATCTGCTCCCTTACAGGGAGTGAAGAAACAGAGAGCTGTG 1242
QY 341 TyrIleAlaIlyAspHisIleuAspIlyIlyIlyValIleSerGluProGlyIlyValIle 360
DB 1243 TACATTGCCAAGATCCTTAACAGAAAGAAAGAAAGCAATCTGAGCCTGAAAAGTTATA 1302
QY 361 ValLeuValAsnIlyValIleuLeuValGluGlnLeuPheArgIlyGluPheGlnProPhe 380
DB 1303 GTTCTTGTCAATAGGATCTGCTAGTTGAACAGCTTCTCCGACAGAGATTCCACACATT 1362
QY 381 LeuIlyIySerTTrpThrArgValIleGlyLeuSerGlyAspThrGlnLeuIlyIleSerPhe 400
DB 1363 TTGAAGAAATGTATGTGTATTTGATTAAGTGTGATACCACACTGAATAATATCATTT 1422
QY 401 ProGluValIlySerCysAspIleIleIleSerThrAlaGlnIleuGluAsnSer 420
DB 1423 CCAGAAATTGTCAAGTCTGTGATATTATATCAAGTCAAGCTCAAAATCCTTGAAACCTCC 1482
QY 421 LeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuIle 440
DB 1483 CTCTTAACTTGGAAATATGAGAAAGATGCTGGTTCATTTGACATCTTCCCTCATTT 1542
QY 441 IleIleAspGluCysHisIleThrAsnIlyGluAlaValIlyThrAsnGlnIleMetArgHis 460
DB 1543 ATCATTTGATGAATGTATCATCACCAACAAAGAAAGCGTGTATATATATCATCTGAGCGCAT 1602
QY 461 TyrLeuMetGlnIlyLeuIlyAsnAsnArgLeuIlyValGluAsnIlyAspProValIlePro 480
DB 1603 TATTTATGACAGAAAGTTGAAACCAATAGACTCAAGAAAGAAACCAACAGATTTCC 1662
QY 481 LeuProGlnIleuGlnIlyLeuThrAlaSerProGlyValGlyIlyValIleThrIlyGlnAla 500
DB 1663 CTTCCTCAATACTGGGACTTACAGCTTCACTCGTGTGGAGGGGCCACAGAAAGCAAGCC 1722
QY 501 IlyAlaGluGlnHisIleLeuIlyIleuCysAlaAsnLeuAspAlaPheThrIleIyThr 520
DB 1723 AAGCTGAAGAACACATTTTAAACATATGTGCCAATCTTGATGCAATTTCTATTAAACT 1782
QY 521 ValIlyGluAsnLeuAspGluLeuIlyAsnGlnIleGlnIlyProCysIlyIlyPheAla 540
DB 1783 GTTAAAGAAACCTTATCATCACTGAAACCAAAATACAGAGCCATGCAAGAAAGTTTGC 1842
QY 541 IleAlaAspAlaThrArgGluAspProPheIlyGluIlyLeuLeuGlnIleMetThrArg 560
DB 1843 ATTGCAGATGCCAACAGAGAAATCCATTAAAGAAACCTTAAATTAATGACAAAG 1902
QY 561 IleGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGluGln 580
DB 1903 ATTCAAACTTATGTTCAAAATGAGTCCAAATGTCAGATTTTGAACTCAACCTTATGAACA 1962
QY 581 TrpAlaIleGluMetClyIlyIlyIlyValAlaIlyIlyGlyIlyAsnArgIlyGluArgValCys 600
DB 1963 TGGGCAATTCAAATGGAAAAAGCTGCAGAAAGAAAGAAATGCAGAAAGAACTGTTGT 2022
QY 601 AlaGluHisIleuArgIlyIlyIlyGlnAlaIleuGlnIleAsnAspThrIleArgMetIle 620
DB 2023 GCAGAACTTTTGAAGAAATGACATGAGCCCTTCAAAATTAATGACAAATTCGAATGATA 2082
QY 621 AspAlaIlyThrHisIleuGlnThrPheTyrAsnGluGluIlyAspIlyIlyPheAlaVal 640
DB 2083 GATGCGTATATCATCTTGAACCTTCTATTAAGAAAGAAAGATTAAGAAAGTTTGCAGTCC 2142
QY 641 IleGluAspAspSerAspGluGlyIlyAspAspGluTyrCysAspGluIlyAspGluAspGlu 660
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QY LeuLeuLeuSerThrLeuGluLeuGlyVal1TrpHisLeuGlyTrpThrArgGluPheVal1 80
Db CTGCTGCTGAGCACCTTGAGAAAGGAGTCTGGCACTTGATTGCACTCGGAAATTCGATG 462
QY 81 GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyMetLeuProGluLeuThr 100
Db GAGGCCCTCCGAGAACCGGACGCCCTCGCGCCGCTACATGAACCTTGAGCTCAGG 522
QY 101 AspLeuProSerProSerPheGluAAsnAlaHisAspGluTyLeuGlnLeuLeuAAsnLeu 120
Db GACTTGCCCTCTCCATCGTTTGAAACGCTCATGATGAATATTTCCAACTGCTGAACCTC 582
QY 121 LeuGlnProThrLeuValAspTySLeuLeuValArgAspValLeuAspTyCyMetGlu 140
Db CTTTCAAGCCCACTCTGGTGGCAAGCTTTAGTAAAGAGCTCTTGATTAAGTCATGAG 642
QY 141 GluGluLeuLeuThr11LeGluAspArgAsnArg11LeAlaAlaAgLuAsnAsnGlyAsn 160
Db GAGGAACGTGTGCAATGTCAGACAGAAACCGGATTTGCTGTCAGAAAAACAATGGAAT 702
QY 161 GluSerGlyValArgGluLeuLeuLeuValArg11LeValGlnGlyGluAsnTrpPheSerAla 180
Db GAATTCAGGTGTAAAGAGACTTAAAGAGATTGTGCAAGAAAGAACTGGTTCTTGCA 782
QY 181 PheLeuAsnValLeuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer 200
Db TTTCTGAATGTTCTTGTCTGCAACAGGAACAATGAACCTTGCCAAAGTTAAACAGCTCT 822
QY 201 AspCySerSerGluSerAsnAlaGlu11LeGluAsnLeuSerGlnValAspGlyProGlnVal 220
Db GATTGCTCAGAAAGCAATGACAGATGAGAAATTTTACAAAGTTGATGCTCTCAAGTG 882
QY 221 GluGluGluLeuLeuSerThrThrValGlnProAsnLeuGluLeuGluVal1TrpGlyMet 240
Db GAAAGCAACTTTTTCACACCAACGTTCCACCAATCTGAGAAAGAGAGCTGGGGCATG 942
QY 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValAspGluSerAspThr 260
Db GAGAAATACATCATCAGAAATCATCTTTTGACAGATTCTTGTAGTTTCAGAAATCAGACACA 1002
QY 261 SerLeuAlaGluGlySerValSerCySLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
Db AGTTTGGCAGAAAGAGTGCACCTGCTTGAATGAAGCTTGAGACATTAACACACATG 1062
QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
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QY 301 SerProGluProGluLeuGlnLeuArgProTyrglnMetGluValAlaGlnProAlaLeu 320
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QY 321 GluGlyValAsnAla11Le11LeCySLeuProThrGlySerGlyTyThrArgValAlaVal 340
Db GAAAGGAAAGAAATCATCATCTGCTCCCTTACAGGGAGTGGAAGAACCAAGAGGCGTT 1242
QY 341 Tyr11Ala11AspHisLeuAspTySLeuAspTySLeuValAspGluProGluTyLeuVal11Le 360
Db TACATGGCCAAAGATCATCTTAACACAAAGAAAAACATCTGAGCCTGGAAGAAATATA 1302
QY 361 ValLeuValAsnValSLeuLeuValGluGlnLeuPheArgGluPheGlnProPhe 380
Db GTTCTTGTCAAATAAGTACTGCTAGTTGAACAGCTTTCGCAAGGAGTTCCAAACCATTT 1362
QY 381 LeuLeuLeuSerTrpTyArgVal11LeGlyLeuSerGlyAspThrGlnLeuVal11LeSerPhe 400
Db TTGAAGAAATGCTATCTGTTATTTGATTAAGTGTATATCCCAACGAAATAATCATTTT 1422
QY 401 ProGluValValAspSerCyAspAla11Le11LeSerThrAlaGln11LeGluAsnSer 420
Db CCGAAGTTTCAAGTCTGTGATATTAATATCATGATCAAGCTCAAAATCTTGAAATCTCC 1482
QY 421 LeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeu11Le 440

Db 1483 CTTTAAACTTGAAAAATGAGAAAGTGTGGTTCAATGTGCACATTTTCCCTCATTT 1542
QY 441 11Le11AspGluCyHisHis11ThrAsnGlyValAla11TyAsnAsn11MetArgHis 460
Db ATCATTTGAATGATTCATCATCACACCAAGAAAGAGCTGTATATATATCATCATGAGGCAT 1602
QY 461 TyrLeuMetGlnTySLeuTySLeuAsnAsnArgLeuTySLeuGluAsnTySProVal11Pro 480
Db TATTTGATCAGAAAGTTGAAAAACAATAGACTCAAGAAAGAAACAACCAAGTGAATTC 1662
QY 481 LeuProGln11LeGluGlyLeuThrAlaSerProGluValGlyValAlaThrTySAla 500
Db CTTCTCAGATCTGGAGCTTAACGCTTCACTGCTGTGGAGGGGCCAGAAAGCAAGCC 1722
QY 501 TySAlaGluGluHis11LeuTySLeuCySAlaAsnLeuAspAlaPheThr11LeTySThr 520
Db AAGCTGAAGAAACACTTTTAAACATATGTCCAATCTTGATGCAATTTCTATTAACCT 1782
QY 521 ValTySLeuAsnLeuAspGlnLeuTySAsnGln11LeGlnGluProCySLeuTySLeuPheAla 540
Db GTTAAAGAAACCTTGATCATCACTGAAGAAACCAAAATACAGAGCCATGCAAGAAATTTGCC 1842
QY 541 11Le11AspAla11ThrArgGluAspProPheTySLeuLeuGln11LeMetThrArg 560
Db ATTCAGATGCAACCAAGAAAGATCTTAAAGAAACCTTTAGAAATTAATGACAAAG 1902
QY 561 11LeGlnThrTyrglnMetSerProMetSerAspPheGlyThrGlnProTyrglnGln 580
Db ATTCAAACTTATTTGTCAAAATGAGTCAATGTCAAGATTTTGAACCTCAACCTTAAGAAACA 1962
QY 581 TrpAla11LeGlnMetGluTySLeuValAlaTySLeuGlyAsnArgLeuArgValCyS 600
Db TGGGCATTTCAATGAGAAAAAAGCTGCAAAAAGAAAGAAATCGCAAGAACCTGTTGT 2022
QY 601 AlaGluHisLeuArgTySLeuArgValAlaLeuGln11LeAsnAspThr11LeArgMet11Le 620
Db GCAGAACATTTGGAAAGTACATGAGGCCCTTACAAATTAATGACAAATTCGAATGATTA 2082
QY 621 AspAlaTyrglnThrHisLeuGlnThrPheTyrglnGluGluTySLeuAspTySLeuPheAlaVal 640
Db GATGCTATATCATCATTTGAACTTTCTATTAATGAAGAAAGATTAAGAAATTTGCAAGTC 2142
QY 641 11LeGluAspAspSerAspGluGlyGlyAspAspGluTyrglnAspGluAspGlu 660
Db ATGAAGATGATGTATGATGAGGTGTGATGATGATGATGATGATGATGATGATGATGATG 2202
QY 661 AspAspLeuTySLeuProLeuTySLeuAspGluThrAspAspPheLeuMetThrLeuPhe 680
Db GATGATTTTAAAGAAACCTTGAAACCTGATGAAGAAACAGATGATTTCTCATGACTTTATTT 2262
QY 681 PheGluAsnAsnTySLeuTySLeuArgLeuAlaGluAsnProGluTyrglnAsnGluTyS 700
Db TTTGAAAAACAATTAATTTGTAAGAAAGCTGGTGGAAACCCAGAAATATGAATTAAGAAAG 2322
QY 701 LeuThrTySLeuArgAsnThr11LeMetGluGlnTyrglnThrArgThrGluGluSerAlaArg 720
Db CTGACCAAAATTAAGAAATACATATGAGCAATATATCTAGAGCTGAGAAATCAGACAGA 2382
QY 721 Gly11Le11LePheThrTySLeuThrArgGlnSerAlaTyrglnLeuSerGlnTrp11LeThrGlu 740
Db GGATATATCTTTTCAAAACACGACAGAGCTGAATGCGCTTTCCAGATGATTAATCTGAA 2442
QY 741 AsnGluTySLeuPheAlaGluValGlyValTySLeuHisHis11Leu11LeGlyAlaGlyHisSer 760
Db AATGAAAAATTTCTGTAAGTGAAGTCAAGGCCACATGTGATTTGAGAGCTGAGCACAGC 2502
QY 761 SerGluPheLeuAspProMetThrGlnAsnGluGlnTySLeuVal11LeSerTySLeuPheArgThr 780
Db AGTGAAGTTCAAAACCATGACACAGAAATGAACAAAGAAAGTCAATGTGTAATTTTCCGACT 2562
QY 781 GlyTySLeuHisLeuLeuLeu11LeAlaThrThrValAlaGlnGluGluLeuAsp11LeTySLeu 800

1151 TTTCTGAATGTTCTTGTCAACAGGAAACAATGAACCTTCCMAAGTTAAACAGCCTCT 1210
Qy AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGluProGlnVal 220
Db 1211 GATGCTCAGAAAGCAATGAGATTCAGAAATTTATCACAACTTGATGCTCTCAAGTG 1270
Qy 221 GluGluGlnLeuLeuSerThrValGlnProAsnLeuGlnLysGlnValTyrGlyMet 240
Db 1271 GAAAGCAACTTCTTCAACCAACAGTTACAGCAAACTCGAGAAAGAGGCTGGGGCATG 1330
Qy 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValValSerGluSerAspThr 260
Db 1331 GAGAAATACATCAACAATCATCTTTTGACAGATTCTGTGATTTCAAGATACACAC 1390
Qy 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
Db 1391 AGTTTGCGAGAGAGAGAGTGTACAGCTGTTAGATGAAGTCTTGACATTAACACCAATG 1450
Qy 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGlnAsnValAlaAlaArgAla 300
Db 1451 GCGAGGATTCAGGCAACATGGGAGATTCAGATGAAGAGAAATGGCGCAGCAAGCA 1510
Qy 301 SerProGluProGluLeuGlnLeuAlaGProTyrGlnMetGlnValAlaGlnProAlaLeu 320
Db 1511 TCCCGCGAGCCAGAACTCCAGCTCAGGCTTACCAATGAGAAAGTTGCCAGCCAGCTTG 1570
Qy 321 GluGlyLysAsnIleIleIleCysLeuProThrGlySerGlyLysThrArgValAlaVal 340
Db 1571 GAAAGGAGAAATATCATCATCTGCTCCCTCAAGGAGTGGAAGAAACCAAGAGGGCTGT 1630
Qy 341 TyrIleAlaLysAspHisLeuAspLysLysLysLysAlaSerGluProGlyLysValIle 360
Db 1631 TCATGTCGCAAGATCATCTTAGCAAGAGAAABAAAGCATCTGAGCTGGAAAAAGTTATA 1690
Qy 361 ValLeuValAsnLysValLeuLeuValGluGlnLeuPheArgLysGluPheGlnProPhe 380
Db 1691 GTTCTGTCAATGAAGTACTGCTAGTTGAACAGCTCTCCGCAAGGAGTTCCAAACCATTT 1750
Qy 381 LeuLysLysThrTyrTrpArgValIleGlyLeuSerGlyAspThrGlnLeuLysIleSerPhe 400
Db 1751 TTGAAGAAATGATGATGTTATTTGATTAAGTGATATCCCACTGAAAAATATCATCTT 1810
Qy 401 ProGluValValLysSerCysAspIleIleIleSerThrAlaGlnIleLeuGluAsnSer 420
Db 1811 CCGAAGTTGTCAAGTCCGTGATATTTATATCATGATCAAGCTCAAACTCTTGAACCTCC 1870
Qy 421 LeuLeuAsnLeuGlnAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuIle 440
Db 1871 CTCTTAAACTTGAAAAATGAGAAAGATGCTGCTGTTCAATTTGTCAGACTTTTCCCTCAT 1930
Qy 441 IleIleAspGluCysHisIleThrAsnLysGlnAlaValTyrAsnAsnIleMetArgHis 460
Db 1931 ATCATTTGATGAATGTCATCACCAACAAGAGAGCTGATATTAATACATCAAGAGCAT 1990
Qy 461 TyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysLysGlnAsnLysProValIlePro 480
Db 1991 TATTTGATGCAAGAGTTGAAAAACAATAGACTCAAGAAAGAAAAACAACAGATGCC 2050
Qy 481 LeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGlyValAlaThrLysGlnAla 500
Db 2051 CTTCCTCAGATACCTGGGACTTAACAGCTTCACTGTGTTGAGAGGGCCAGAAAGCAAGCC 2110
Qy 501 LysAlaGlnGlnHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThrIleLysThr 520
Db 2111 AAGCTGAAGAAACAATTTTAAACTATGTGCCAATCTTATGATGATTTACTTTTAAACT 2170
Qy 521 ValLysGlnAsnLeuAspGlnLeuLysAsnGlnIleGlnGlnLupProCysLysPheAla 540
Db 2171 GTTAAAGAAAACTTGATTCATGAAAAACAATACAGAGCCATCAAGAAAGTTTGCC 2230
Qy 541 IleAlaAspAlaThrArgLysAspProPheLysGlnLysLeuLeuGlnIleMetThrArg 560

2231 ATTGCAGATCAACACAGAGAAGATCCATTTAAAGAAAACTCTAGAAATATATGACAAG 2290
Qy 561 IleGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGlnGln 580
Db 2291 ATTCAAACTTATTTGTCAAATATGAGTCCAAATGTCAGATTTTGGAACTCAACCTTATGAACA 2350
Qy 581 TrpAlaIleGlnMetGlnLysLysAlaAlaLysLysGlyLysAsnArgLysGlnValCys 600
Db 2351 TGGCCATTCAAATGGAAGAAAAAGCTGCAAAAGAAATCGCAAGAAACGTGTTGT 2410
Qy 601 AlaGlnHisLeuArgLysTyrAsnGlnAlaLeuGlnIleAsnAspThrIleArgMetIle 620
Db 2411 GCGAAGCAATTTAGAGAGATACATAGAGGCCCTTACAAATTAATACACCAATTCGAATGAT 2470
Qy 621 AspAlaTyrThrHisLeuGlnLuthrPheTyrAsnGlnGlnLysAspLysPheAlaVal 640
Db 2471 GATGCTATATCATCTTGAACCTTTCTATTAATGAAGAGAAAGATTAAGAAATTTGCAGCT 2530
Qy 641 IleGluAspAspSerAspGluGlyGlyAspAspGluTyrCysAspGluAspGluAspGlu 660
Db 2531 ATGAAGATGATATGATAGAGGTGGTGTGATGATGATATTTGATGATGATGAAGATGAG 2590
Qy 661 AspAspLeuLysLysProLeuLysLeuAspGluThrAspArgPheLeuMetThrLeuPhe 680
Db 2591 GATGATTTAAAGAAACCTTTGAACCTGATGAACAGATAGATTTCTCATGACTTTATTT 2650
Qy 681 PheGluAsnAlaLysMetLeuLysArgLeuAlaGluAsnProGluTyrGlnAsnGlnLys 700
Db 2651 TTTGAAABACAATTAATGTTGAAGAAAGCTGGCTGGAACCCAGAAATATGAAGAAAG 2710
Qy 701 LeuThrLysLeuArgAsnThrIleMetGlnGlnTyrThrArgThrGlnGlnSerAlaArg 720
Db 2711 CTGACCAAAATTAAGAAATCCAAATGAGCAATATACATGAGCTAGAGAAATACAGACGA 2770
Qy 721 GlyIleIlePheThrLysThrArgLysAsnArgAlaTyrAlaLeuSerGlnTrpIleThrGln 740
Db 2771 GGAATATCTTTACAAABACACAGACAGTGCATAGCGCTTTCCAGTGGATTAAGTGA 2830
Qy 741 AsnGlnLysPheAlaGlnValGlyValLysValHisIleLeuIleGlyAlaGlyHisSer 760
Db 2831 AATGAABAAATTTGCTGAAGTAGAGTCAAAAGCCACATCTGATGAGCTGACACAGC 2890
Qy 761 SerGluPheLysProMetThrGlnAsnGlnGlnLysGlnValIleSerLysPheArgThr 780
Db 2891 AGTGAAGTCAAAACCCATGACACAGATGAACAAAGAAAGTCAATGTAATTTCCGACT 2950
Qy 781 GlyLysIleAsnLeuLeuIleAlaThrThrValAlaGlnGlnLysLeuAspIleLysGln 800
Db 2951 GGAABAAATTAATCTGCTTATCGTACACAGATGCGAAGAGAGTCTGATATTAAGAA 3010
Qy 801 CysAsnIleValIleArgTyrGlyLeuValThrAsnGlnIleAlaMetValGlnAlaArg 820
Db 3011 TGTAACATTTGTTATCCGTTATAGTGTCTGTCAACCAATGAATACCATGTCAGAGCCGT 3070
Qy 821 GlyArgAlaArgAlaAspGluSerThrTyrValLeuValAlaHisSerGlySerGlyVal 840
Db 3071 GGTGAGCCGAGACGTATGAGACACTACGCTGCTGTGCTCACAGTGTTCAGAGATT 3130
Qy 841 IleGlnHisGlnThrValAsnAspPheArgGlnLysMetMetTyrLysAlaIleHisCys 860
Db 3131 ATGAAACATGAGACATTAATGATTTCCGAGAAABATGATGATTAAGCTTATACATTTGT 3190
Qy 861 ValGlnAsnMetLysProGluGlnTyrAlaHisLysIleLeuGlnLeuGlnMetGlnSer 880
Db 3191 GTTCABAAATATGAAACACAGAGATGTGTCATTAAGATTTTGAATTAACAGATGCAAGT 3250
Qy 881 IleMetGlnLysLysMetLysThrLysArgAsnIleAlaLysHisTyrLysAsnAsnPro 900
Db 3251 ATATGGAAGAAAGAAATGAAACCAAGAGAAATATGTCCAAGCATTAACAAGAAATTAACCA 3310
Qy 901 SerLeuIleThrPheLeuCysLysAsnCysSerValLeuAlaCysSerGlyGlnAspIle 920
Db 3311 TCACATAATACTTTCTTGCAAAAAATGACAGTGTGCTAGCCTGTGCTGGGGAAGATATC 3370

QY 921 HisValIIEGLuIuysMeThiShiValaAsnMeThProGluPheIysGluLeuTyrIle 940
Db 3371 CATGTAAATGAGAAATGCAATCGTCAATATATACCCCGAATTCAGAGACTTTACATT 3430
QY 941 ValArgGluAsnLysAlaLeuGlnLysCysAlaAspTyrGlnIleAsnGlyGluIle 960
Db 3431 GTTAGAGAAACAAACACTGCAAAAAGAGTGTGCCGACTATCAAAATTAATGTGAATC 3490
QY 961 IIECysLysGlyGlyGlnAlaTTPGlyThrMetMetValHisLysGlyLeuAspLeuPro 980
Db 3491 ATCTGCAAAATGTGCGCAGCTTGCGGAAACATATGCTGCACAAAGCTTAAATTGCCCT 3550
QY 981 CysLeuLysIleArgAsnPheValValIlePheLysAsnAsnSerThrLysLysGlnTyr 1000
Db 3551 TGTCTCAAAATTAAGAAATTTGTAGTGTGTTTCAAAATTAATTCACAAAGAAACAAATAC 3610
QY 1001 LysLysTyrValGluLeuProIleThrPheProAsnLeuAspTyrSerGlyCysCysLeu 1020
Db 3611 AAAAATGGGTAGAAATTACTATCACATTTCCCAATCTTGACTATTCAGAAATGCTGTATA 3670
QY 1021 PheSerAspGluAsp 1025
Db 3671 TTTAGTGAATGAGGAT 3685
RESULT 9
ID ABA04908 standard; cDNA; 3372 BP.
AC ABA04908;
XX 05-MAR-2002 (first entry)
DT Human RNA helicase RH16 coding sequence.
DE
XX Human, RH16; RNA helicase; cytosolic; virucide; anti-HIV;
KW immunosuppressive; immunostimulatory; antirheumatic; antidiabetic;
KW antiarteriosclerotic; osteopathic; antidiabetic; hepatotropic;
KW antiinflammatory; cancer; infection; HIV; hepatitis; genetic disease;
KW autoimmune disease; graft rejection; vaccine; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 155..3232
FT /*tag= a
FT /product= "Human RH16"
XX
PN MO200185955-A1.
XX
XX 15-NOV-2001.
PD
XX 11-MAY-2001; 2001MO-FR001441.
PF
XX 11-MAY-2000; 2000FR-00006030.
PR
XX (ISTA-) ISTAC.
PA (INSP) INST PASTEUR LILLE.
XX
PI Bahr G, Cocude C, Capron A;
XX
XX WPI; 2002-082898/11.
DR P-PSDB; AAM47798.
XX
XX New polypeptide, useful for treating and diagnosing cancer or
PT inflammation, and drug screening; comprises a human polynucleotide
PT homologous to RNA helicase.
XX
XX Claim 7; Page 85-89; 114pp; French.
XX
XX The present sequence is the coding sequence for human RH16. RH16 is a
CC 116kDa protein and has homology to RNA helicases (DEXH box). RH16 and
CC its coding sequence are useful for treating cancer; acute or chronic

CC Infections (especially by HIV or hepatitis B or C); inherited genetic
CC diseases; (auto) immune diseases (particularly rheumatism, arthritis) and
CC arteriosclerosis, osteoporosis and diabetes, but many others listed) and
CC to prevent graft rejection. RH16 and its coding sequence are also useful
CC for inducing, or increasing, the immune response to a vaccine
XX
SQ Sequence 3372 BP; 1157 A; 637 C; 748 G; 830 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 3372
Score: 5285.00 Matches: 1020
Percent Similarity: 99.7% Conservative: 2
Best Local Similarity: 99.5% Mismatches: 3
Query Match: 99.5% Indels: 0
DB: 6 Gaps: 0
US-09-515-363c-2 (1-1025) x ABA04908 (1-3372)
QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20
Db 155 ATGTGAATGGGTATTTCCACAGACGAGATTTCCGCTATCTCATCTCGTTCAGGGCC 214
QY 21 ArgValLysMetTyrIleGlnValGluProValLeuAspTyrLeuThrPheLeuProAla 40
Db 215 AGGTGAAATGATGATCATCCAGGTGGAGCTGTGTGCTGACTGACCTTCTGCTGCA 274
QY 41 GluValLysGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
Db 275 GAGGTGAAGAGACAGATTCAAGAGACGTGCCCTCCGGAAACATGACGACGTTGAA 334
QY 61 LeuLeuLeuSerThrLeuGluLysGlyValTyrPheLysGlyTyrThrArgGluPheVal 80
Db 335 CTGCTGCTAGCACCTTGGAGAAAGGAGCTGGACCTTGTTGACCTGGGAATTCGTG 394
QY 81 GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
Db 395 GAGGCTCTCCGAGAAACCGGACGCCCTCTGCGCGCCGCTGACATGAACTGACCTCACG 454
QY 101 AspLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeu 120
Db 455 GACTTGCCCTCTCCATGTTTAGAAGCGCTCAAGATGAATATCTCAACTGCTGAACCTC 514
QY 121 LeuGlnProThrLeuValAspLysLeuLeuValArgAspValLeuAspLysCysMetGlu 140
Db 515 CTTGACCCCACTCTGTGTGACAAAGCTTCTAGTTAGAGAGCTCTGGATGAATGACGAG 574
QY 141 GluGluLeuLeuThrIleGluAspArgAsnArgIleAlaAlaGluAsnAsnGlyAsn 160
Db 575 GAGGAACCTGTGACAAATGAGAACAGAAACCGGATGCTGTCGCAAAAAACAATGGAAT 634
QY 161 GluSerGlyValArgLysLeuLeuLysArgIleValGlnLysGluAsnTrpPheSerAla 180
Db 635 GAATCAGGTGTAAAGAGCTACTAAAGAAATGTGCACAAAGAAACGCTTCTTGCA 694
QY 181 PheLeuAsnValLeuArgGlnThrArgLysAsnAsnGluLeuValGlnLysLeuThrGlySer 200
Db 695 TTTCTGAATGTTCTTGTCTAAACAGAAACAATGAATCTTGTCCAAAGTTAACAGGCTCT 754
QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220
Db 755 GATGCTCAAGAAAGCAATGACAGATTTGAATTTATCAAGATGATGCTCTCAAGTG 814
QY 221 GluGluGlnLeuLeuSerThrThrValGlnProAsnLeuGluLysGluValTyrPglyMet 240
Db 815 GAAGAGCAACTCTTTCAACACAGCTTGCACCAATCTGAGAAAGAGGTCTGGGGCAGTG 874
QY 241 GluAsnAsnSerSerGluSerPheAlaAspSerSerValValSerGluSerAspThr 260
Db 875 GAGAAATCACTCATCAGAACTCATCTTTGCAAGATTTCTCTGTAGTTCAAGATCAAGACA 934
QY 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
Db 935 AGTTTGCAAGAGAAAGTGTGAGCTGCTTAAGATGAAGTCTTGACATTAACAGCAACATG 994

QY 281 GLYSERASPSERGIYTHMTCGLYSERASPSERASGLIUAANVALAALAAARGA 300
| | | | |
DB 995 GGCAGATGATTCAGGACCAATGGAGATGATTCAGATGAAGAGAAATGGCAGCAAGCA 1054
QY 301 SERPROGLUPROGLIULEUGIULEUARGPROTYRGIMETGLIUALAAGIUPROALAEU 320
| | | | |
DB 1055 TCCCGGAGCCAGAACTCCAGCTCAGGCTTACCAATAGGAAGTTCCAGCCAGCCCTTG 1114
QY 321 GIUGIYLYASNIIEIIEIIECYBLEUPROTHRGILYSERGIYLYETHRARGVALAVAL 340
| | | | |
DB 1115 GAAGAGAAATATCATCATCTGCTCCACAGSAGTGAAGAAACAGAGTGGCTGTT 1174
QY 341 TYRIEALALYEPHISLEUAPPLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 360
| | | | |
DB 1175 TACATTTGCCAAGATACCTTAGCAAGAAAGAAAGAAAGAAAGCAATCTGAGCTGAAAGTTAT 1234
QY 361 VALLEUVALASNLVALLEUVALIUGIULNLEUPHEARGLYSGIUPHEGINPROPE 380
| | | | |
DB 1235 GTTCTTGCAATAGGTAAGTCTAGTTGAACAGCTCTCCGCAAGAGTTCCAAACCATTT 1294
QY 381 LEULYLYSETPHYRTRGVALLIEGIYLEUSERGIYASPTHRGILNLEUYSLIESERPE 400
| | | | |
DB 1295 TTGAAGAAATGGATGATGATTTAGATTAAGTGGATACCAACTGAAATATACATTT 1354
QY 401 PROGLIUALIYASERCYASPIIEIIEIIESETRHALAGIULEUGIUAANSE 420
| | | | |
DB 1355 CCAGAAAGTTGTCAAGCTCTGTATATTATATCATGATCAGCTCAAACTCTGAAACCTCC 1414
QY 421 LEULEASNLUGIUAANGIYGIUAAPRALAGLYVALGINLEUSERAPHESELEUIE 440
| | | | |
DB 1415 CTCTTAACTGGAAATGAGAAAGATGCTGGTTCATTTGCAACTTTTCTTCATTT 1474
QY 441 IIEIIEASPGIUCYHISHIETHRAENLYSGLUALAVALTRYASNAENIIEWCARGHIS 460
| | | | |
DB 1475 ATCATGATGAATGTATCATCACCAACAAAGAGCTGTATATATCATCATGAGCAT 1534
QY 461 TYRLEMECGLINLYSEULYSANASNAARGLEULYLYSEGLIUAANLYSPROVALIIEPRO 480
| | | | |
DB 1535 TATTTGATCCAGAAAGTTGAAABAAACATAGACTCAAGAAAGAAACCAACAGATTTCC 1594
QY 481 LEUPROGLINILEUGIYLEUTHRALASERPROGLIUALIYGLIUALATHRYLSEGINA 500
| | | | |
DB 1595 CTTCCTCAGATACCTGGAGACTTAACAGCTTCACTGGTGGAGGGGCCCAAGAAAGGCC 1654
QY 501 LYSALIGIULNHIETIIELEULYLYSEUCYVALASLEUASPRALAPHETHRIIELYSTHR 520
| | | | |
DB 1655 AAAGCTGAAGAACATTTTAAACATATGTCATCTGATGCATTTACTATTAAACT 1714
QY 521 VALIYEGIUAENLEUPROGLINLEULYSANGLINIEGINIUPROCYSLYLYSPHEALA 540
| | | | |
DB 1715 GTTAAAGAAACCTTGATCACTGAAABAAACCAATACAGAGCCATGCAAGAAAGTTGCC 1774
QY 541 IIEALIASPRALATHRARGIUAAPROPHELYSGIULYSELEUGIUIEMECTHARG 560
| | | | |
DB 1775 ATTCAGATGCAACCAAGAGATTCATTTAAAGAGAACTTCTAGAAATTAAGACAGG 1834
QY 561 IIEGLIETHRYRCYEGINMETSERPROMETSERASPHREGIYTHRGINPROTYRGIULIN 580
| | | | |
DB 1835 ATTCAAACTTATGTCAAATGAGTCCATGTCAGATTTTGGAACTCAACCTATGACAA 1894
QY 581 TTPDALIEGINMETGIULY 600
| | | | |
DB 1895 TGGGCCATTCAAATGGAAAAAAGCTGCAGAAAGAGAAATGCAAGAAAGAAAGTTGTT 1954
QY 601 ALAGIULHIELEULY 620
| | | | |
DB 1955 GCAGAACATTTGAGAAAGTCAATTAAGGCCCTTACCAATTTATGACCAATTTCCAAATGAT 2014
QY 621 ASPRALATHRYTHRIIELEUGIUTHRPHETRYRANGIUGIULYLYLYLYLYLYLYLYLYLY 640
| | | | |
DB 2015 GATGCGATATACATCTTGAACCTTTCTATATGAAGAAAGAAAGTTTGGAGCTC 2074

QY 641 IIEGLIUAAPSPERASPGIULIYGLIYASAPRGIULTRYCYVASAPGLYASPGIUAAPROGL 660
| | | | |
DB 2075 ATAGAAAGATGATAGATGAGAGGCTGTATGATGATTTGATGATGATGATGATGATGATG 2134
QY 661 ASPRAPPLY 680
| | | | |
DB 2135 GATGATTTAAAGAAACCTTGAAACTGGATGAAACGATGAAATTTCTCATGACCTTATTT 2194
QY 681 PHEGLIUAENASNLMECTLEULY 700
| | | | |
DB 2195 TTTGAAACCAATTAATGTTGAAAGGCTGCTGTAAGAACCCAGAAATATGAAATGAAAG 2254
QY 701 LEUTHRYLYSEULYARGANETHRIIEWCETGIUGINTYRTHARGTGHUGIUSERALAA 720
| | | | |
DB 2255 CTGACCAATTAATTAAGAAATCCATTAATGAGCAATATACAGAACTGAGGAATCAGACACA 2314
QY 721 GIYIIEIIEPHEETHRYRARGINSERALATRYALALEUSERGINTRPIIETHRGIU 740
| | | | |
DB 2315 GGAATATCTTTTACAAACACAGACAGAGTGCATATGCGCTTTCCAGTGGATTTACTGA 2374
QY 741 AENGILYLYSPHEALAGIULVALIYVALIYVALIYVALIYVALIYVALIYVALIYVALIY 760
| | | | |
DB 2375 AATGAAAAATTTGCTGAAGTACAGAGTCAAAAGCCCAACATCTGATTTGAGACTGACACAC 2434
QY 761 SERGIUPHELYPROMETHTRGIDANGIUGIULYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 780
| | | | |
DB 2435 AGTGAAGTTCAAAACCATGACACAGATGAACAAAGAAAGTATTAATTAATTTGCGACT 2494
QY 781 GIYLY 800
| | | | |
DB 2495 GGAATATTAATCTGCTTATCCCTACACAGTGGCAAGAAAGCTGTGATTTAAAGAA 2554
QY 801 CYASNIIEVALIIEARGTYRGIYLEUVALIETHRANGIULIIEALAMECVAGIUALAARG 820
| | | | |
DB 2555 TGTAACTATTGATCCGTTATGCTATGCTCCGTCACCAATGAATGAGCATGCTCCAGGCTCG 2614
QY 821 GIYARGALATARGALAAAPROGLIULYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 840
| | | | |
DB 2615 GGTGAGCCAGAGCTGATGAGAGCACTTACGCTCGTGGTTCACACAGTGGTTCAGAGAGTT 2674
QY 841 IIEGLIULHIEGLIUTHRYALASAPRPHEARGSIULYVMECTEULYLYLYLYLYLYLYLY 860
| | | | |
DB 2675 ATCGAACTGGAACGTTATATGATTTCCAGAAAGATATGATTAATACCTTATCTTT 2734
QY 861 VALIINAMMECTLYSEPROGLIULYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 880
| | | | |
DB 2735 GTTCAABAAATATGAACCAAGAGATATGCTCATTAAGATTTTGGAAATTAAGATGCAAG 2794
QY 881 IIEWCETIULY 900
| | | | |
DB 2795 ATATATGAAAGAAAGAAATGAAACCAAGAGAAATATTTGCCAACATTTAACAGAACCA 2854
QY 901 SERLEUIIEETHRPHENUCYLY 920
| | | | |
DB 2855 TCACTATATATCTTCTTTGCAAAACCTGCAAGTGGCTGCTGTTCTGGGAAAGTATTC 2914
QY 921 HIEVALIIEGLIULYMECHIISHIISVALAENMETHTRPROGLIUPHELYSGIULEUTRY 940
| | | | |
DB 2915 CATGTATTTGAGAAATGATCATACGTCATATGACCCAGAAATTCAGAACTTTATCATTT 2974
QY 941 VALIARGIUAENLY 960
| | | | |
DB 2975 GTTAAAGAAACCAAGACCTGCAAGAAAGATGTCGCACTATTCATTAATGATGTTAAATC 3034
QY 961 IIECYLYSECYGLIYGINIATTPRGIYTHRMETMEVALIHSIYLYSGIYLEUASPRLEUPRO 980
| | | | |
DB 3035 ATCTGAAATGTCGCGGCTTGGGAAACAAATGATGCTCACAAAGGCTTTAGATTTGGCT 3094
QY 981 CYLEULY 1000
| | | | |
DB 3095 TGTCTCAAAATTAAGAAATTTTGTAGTGTCTTCAAAAATATATTCACAAAGAAACAAATAC 3154
QY 1001 LYSLYSETPYVALIGIULEUPROILETHRPHETROENLEUASPTYRSERGIUCYVSEU 1020

Db	3155	AAAAAAAAAGTGGAGAGANTTACCTTACATCTTCCCATCTTGACTATTCAGATGCTGTTTA	3214
Qy	1021	PheserAepgiuAep	1025
Db	3215	TTTAGTGATGAGAT	3229
RESULT 10			
ADCC30823			
ID	ADCC30823	standard; cDNA; 3446 BP.	
AC	ADCC30823;		
XX			
DT	18-DEC-2003	(first entry)	
XX			
DE	Human novel cDNA sequence, SEQ ID NO:905.		
KW	Human; diagnostic; drug screening; forensics; gene mapping;		
KW	biodiversity assessment; Parkinson's disease; Alzheimer's disease;		
KW	neurodegenerative diseases; anaemia; platelet disorder; wound; burns;		
KW	ulcers; osteoporosis; autoimmune disease; cancer;		
KW	molecular weight marker; food supplement; antiparkinsonian; nootropic;		
KW	neuroprotective; antihaemic; anticoagulant; thrombolytic; vulnerary;		
KW	antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;		
KW	gene therapy; gene; ss.		
XX			
OS	Homo sapiens.		
PN	WO2003029271-A2.		
XX			
PD	10-APR-2003.		
XX			
XX	24-SEP-2002; 2002WO-US030474.		
PR	24-SEP-2001; 2001US-0324631P.		
XX			
PA	(HYSE-) HYSEQ INC.		
PI	Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;		
PI	Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;		
PI	Haley-Vicente D, Drmanac RT;		
XX			
DR	WPI; 2003-371981/35.		
DR	P-PSDB; ADCC31794.		
PT	New polynucleotide and polypeptide useful for diagnosing, preventing or		
PT	treating conditions such as neurodegenerative diseases, anemias, platelet		
PT	disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or		
PT	cancer.		
PS	Claim 1; SEQ ID NO 905; 1185bp; English.		
XX			
CC	The invention relates to 971 novel human cDNA sequences (ADC29919-		
CC	ADC30869) and the polypeptides they encode (ADCC30850-ADCC31860). The		
CC	invention also relates to nucleic acid sequences over 99% identical with		
CC	the novel human cDNAs. The invention additionally encompasses expression		
CC	vectors and host cells comprising a nucleic acid of the invention; the		
CC	recombinant production of a polypeptide of the invention; an antibody		
CC	against a polypeptide of the invention; a method of detecting		
CC	polynucleotides or polypeptides of the invention; and methods of		
CC	identifying a compound which binds to a polypeptide of the invention. The		
CC	invention further discloses methods of preventing, treating or		
CC	ameliorating a medical condition; kits comprising polynucleotide probes		
CC	and/or monoclonal antibodies for carrying out the methods of the		
CC	invention; methods for the identification of compounds that modulate the		
CC	expression or activity of the polynucleotide and/or polypeptide; and 767		
CC	contig sequences corresponding to the cDNA sequences of the invention		
CC	(ADCC1861-ADCC32627) and the polypeptides encoded by the contigs (ADCC32628		
CC	-ADCC33394). The nucleic acids and polypeptides of the invention are		
CC	useful in diagnostics, drug screening, forensics, gene mapping, in the		
CC	identification of mutations responsible for genetic disorders or other		
CC	traits, for assessing biodiversity, and in producing many other types of		
CC	data and products dependent on DNA and amino acid sequences. They are		

	CC	also used for treating diseases such as Parkinson's disease, Alzheimer's
	CC	disease and other neurodegenerative diseases, anaemia, platelet
	CC	disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
	CC	cancer. The nucleic acids may also be used as hybridisation probes or
	CC	primers, and in the recombinant production of a protein. The polypeptides
	CC	are also useful in generating antibodies, as molecular weight markers,
	CC	and as food supplements. The present sequence represents a specifically
	CC	claimed human cDNA sequence of the invention. Notes: The sequence data from
	CC	this patent did not form part of the printed specification, but was
	CC	obtained in electronic format directly from WIPO at
	XX	ftp.wipo.int/pub/published_pct_sequences.
SQ	Sequence 3446 BP; 1184 A; 649 C; 772 G; 841 T; 0 U; 0 Other;	
	Alignment Scores:	
Pred. No.:	0	Length: 3446
Score:	5285.00	Matches: 1020
Percent Similarity:	99.7%	Conservative: 2
Best Local Similarity:	99.5%	Mismatches: 3
Query Match:	99.5%	Indels: 0
DB:	10	Gaps: 0
US-09-515-363C-2 (1-1025) x ADC30823 (1-3446)		
QY	1 MetSerAenGlyTYrSerThraSpoluAnPheuaqTYrLeuIlleSeCySPhenaAla 20	
Db	237 ATGTGAATGGGTATTTCACAGACAGAAATTCCTCACTCATCTCGTTCAGAGGCC 296	
QY	21 ArgValVMeMetTYrIleGlnValGIuProValleAspyTYrLeuthrPheueProAla 40	
Db	297 AGGTGAAAATGTATCATTCAGGTGAGCCTGTGCTGACTGACTTGACCTTTCTGCCTGCA 356	
QY	41 GluValVlSGluGInIleGlnArghThrValalatrNSerGlyYasMeGlnAlaValGIu 60	
Db	357 GAGGTGAAGAAGACAATTCAGAGACAGACGTCCACCTCCGGAAACATGACGACGATTGAA 416	
QY	61 LeuIeuLeuSerThrlengululyselYalTrphIsleuglyTYrThrArgGIuPheval 80	
Db	417 CTGCTGCTGAGACACCTTGAGAGAAAGGAGTCTGGCACCTGTGTGGACTGGGAAATTCGTG 476	
QY	81 GluAlaIeuARgArghThrGIySeProleualAlaIarGlyMecAsnProGIuLeuthr 100	
Db	477 GAGGCCCTCCGAGAACCGGACGCCCTCTGGCCGCCGCTTAACATGAACCTTAGCTCAGC 536	
QY	101 AspleuProSerProSerPheGIuAnAlahIASpGIuTYrLeuGInleuIeuAnleu 120	
Db	537 GACTTGCCCTCTCCATCGTTTGAGAACGCTCATGTATGAATATCTCCAATGGCTGAACCTC 596	
QY	121 LeuGInProthrLeuValAsplysLeuIeuValArGasPvalleuAsplyScyMetGIu 140	
Db	597 CTTGACCCCACTCTGTGTGACAAAGCTTACTGTAGACAGCTTGATTAAGTGCATGAGAG 656	
QY	141 GIuGIuIeuLeuThrlleGIuAspArghAnaAgIIeAlaIaIeGIuAnsnangIyaan 160	
Db	657 GAGGAACGTGTGACAAATTGAACAGAAACCGGATTTGCTGTGCAGAAAACAATGGAAAT 716	
QY	161 GluSerGIyValArgGIuIeuIeuIysArgIleValGIuIySGluAsnTrpPheSerAla 180	
Db	717 GAATRAGGTGTAAAGAGACTACTATAAAAGATTTGTGCAGAAAGAAAACGTGTTCTGTGCA 776	
QY	181 PheIeuAnValleuArghInThrGIyAsnaEngIuIeuValGIuGIuIeuThrGIySer 200	
Db	777 ITTCTGANATGTTCTTCGTCAAACAGAAACAATGAACCTGTCCAAGAGATTAAACAGGCTCT 836	
QY	201 AspCyASerGIuSerAsnAlaGluIleGIuAnleuSerGIuValAspGIyProGIuVal 220	
Db	837 GATTGCTCAGAAAGCAATGACAGAGATTGAGAAATTATATCAACAGTTGATGCTCTCAAGTG 896	
QY	221 GIuGIuGIuIleuIeuSerThrThralGIuProAnleuGIuIySGluValTrpGIyMet 240	
Db	897 GAAAGACAACCTTTCTTCAACACACTTCAGCCAAATCTGAGAAAGAGAGGTCTGGGCGAAG 956	
QY	241 GluIeuAnserSerGIuSerSerPheAlaAspSerSerValValSerGIuSerAspThr 260	

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Db 957 GAGAAATACATCAACAATCATCTTTGACAGATTCTTGAGTTTCAGATATGACACA 1016
QY 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
Db 1017 AGTTGGCAGAGAGAGAGTGCACCTGCTTATGATGAAAGCTTGGACATTAACAGCAACATG 1076
QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
Db 1077 GGAGAGATTACAGGACCATGGAGATGATTGATGAGAGAAATGGGACAGCAAGCA 1136
QY 301 SerProGluProGluLeuGluLeuAlaProGlyGlyMetGlyValAlaGlnProAlaLeu 320
Db 1137 TCCCCGAGGCCAGAACTCCAGCTCAGGCCCTTACCAATGAGAGTTCCCGACGACCTTG 1196
QY 321 GluGluLyAsnMetLeileileCysLeuProThrGlySerGlySerGlyThrArgValAlaVal 340
Db 1197 GAAAGGAAAGATATCATCATCTGCTCCCTACAGGAGTGGAAAAACCGAGTGGCTGTT 1256
QY 341 TyrLeAlaLyAspHisLeuAspLysLysLysAlaSerGluProGlyLysValIle 360
Db 1257 TACATTGCCAAGATCACTTAGCAAGAAAGAAAGAAAGCAATCGAGCTGGAAAGTTAT 1316
QY 361 ValLeuValAsnLysValLeuLeuValGluGluLeuPheArgLysGluPheGlnProPhe 380
Db 1317 GTTCTTGCAATAGGTAGCTAGTTGAACACGCTCTCCGCAAGGAGTTCCAAACATTT 1376
QY 381 LeuLysLysThrTyrArgValIleGlyLeuSerGlyAspThrGlnLeuLysIleSerPhe 400
Db 1377 TGGAAAGAAATGGATGATGTTATTTGATTAAGTGGATATCCCAACCTGAAATATCATTT 1436
QY 401 ProGluValValLysSerCysAspIleIleIleSerThrAlaGlnIleLeuGluAsnSer 420
Db 1437 CCGAAGTTGTCAAGTCCGTGATATTTATTCAGTACAGCTCAAACTCCTTGAAATCTCC 1496
QY 421 LeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuIle 440
Db 1497 CTCCTTAACCTTGAAAAATGAGAAAGATGCTGCTGTTCAATGTCAGACTTTTCTTCATT 1556
QY 441 IleIleAspGluCysHisHisSerThrAsnLysGluAlaValTyrAsnAsnIleMetCArgHis 460
Db 1557 ATCATTTGATGATGATGATCATCACACCAACAAAGAGCGATGATTAATACATCATGAGGCAT 1616
QY 461 TyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysGluAsnLysProValIlePro 480
Db 1617 TATTTGATGAGAAAGTTGAAAAACAATAGACTCAAGAAAGAAACAACACAGATGATCCC 1676
QY 481 LeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGlyGlyAlaThrLysGlnAla 500
Db 1677 CTTCCTCAGATACCTGGGACTTAACAGCTTCACTGCTGTTGGAGGGGCCAGAAAGCC 1736
QY 501 LysAlaGluGluHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThrIleLysThr 520
Db 1737 AAAGCTGAAGAACACATTTTAAACTATATGCTCAATCTTGATGCATTTACTATTTAAACT 1796
QY 521 ValLysGluAsnLeuAspGlnLeuLysAsnGlnIleGlnGlnProCysLysLysPheAla 540
Db 1797 GTTAAAGAAACCTTGAATCACTGAAACCAATACAGAGGCCATGCAAGAAAGTTGCC 1856
QY 541 IleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeuGluIleMetThrArg 560
Db 1857 ATTCAGAGATGCAACAGAGAGATCCATTTAAAGAGAAACCTTAGAAATAATGACAAAG 1916
QY 561 IleGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProGlyGln 580
Db 1917 ATTCAAACTTATGTCAAATGAGTCAATGTCAGATTTTGAACTCAACCTTATGAACAA 1976
QY 581 TrpAlaIleGlnMetGluLysLysAlaAlaLysLysGlyAsnArgLysGluArgValCys 600
Db 1977 TGGGCCATTCAATGGAAAAAAGCTGCAAAAGAAAGAAATGCAAAAGAAAGCTTTGT 2036
QY 601 AlaGluHisLeuArgLysTyrArgGlnAlaLeuGlnIleAsnAspThrIleArgMetIle 620
|||||

Db 2037 GCAGAACATTTAGAGAAATCAATAAGGCCCTTACCAATTAATGACACAAATTGCAATGATA 2096
QY 621 AspAlaTyrThrHisLeuGluThrPheTyrArgGlnGluLysAspLysLysPheAlaVal 640
Db 2097 GATGGGTATATCATCTTGAAACTTTCTATATGAAGAGAAAGATTAAGAAAGTTTGACAGTC 2156
QY 641 IleGluAspAspSerAspGluGlyGlyAspAspGluTyrCysAspGluLysAspGlu 660
Db 2157 ATAGAAAGATGATGATGATGAGGTGGTGTATGATGATTTGATGATGATGAAGATGAG 2216
QY 661 AspAspLeuLysLysProLeuLysLeuAspGluThrAspArgPheLeuMetThrLeuPhe 680
Db 2217 GATGATTTTAAAGAAACCTTGAAACTGATGAAACAGATAGATTTCTCATGACTTTATTT 2276
QY 681 PheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnProGluTyrGluAsnGluLys 700
Db 2277 TTTGAAACCAATTAATGTTGAAAGGCTGGCTGAAAAACCGAATATGAAATGAAAG 2336
QY 701 LeuThrLysLeuArgAsnThrIleMetGluGlnTyrThrArgThrGluGluSerAlaArg 720
Db 2337 CTGACCAAAATTAAGAAATGCAATATGAGCAATATACTAGGACTGAGGAATCAGACGCA 2396
QY 721 GlyIleIlePheThrLysThrArgGlnSerAlaTyrAlaLeuSerGlnTrpIleThrGlu 740
Db 2397 GGAATATCTTTACAAAAACGACAGAGTGCATATGCCCTTTCCAGTGCATTTACTGAA 2456
QY 741 AsnGluLysPheAlaGluValGlyValLysAlaHisHisLeuIleGlyAlaGlyHisSer 760
Db 2457 AATGAAAAATTTGCTGAAGTATAGAGATCAAGGCCACCATCTGATTGGAGCTGGACACAGC 2516
QY 761 SerGluPheLysProMetThrGluAsnGluGlnLysGluValIleSerLysPheArgThr 780
Db 2517 AGTAGATTCAAAACCCATGACAGATGAAACAAAGAAAGTCAATTAATTTCCGCACT 2576
QY 781 GlyLysIleAsnLeuLeuIleAlaThrThrValAlaGluGluGlyLeuAspIleLysGlu 800
Db 2577 GGAATAATTAATCTGCTTTACCTACACAGTGGCGAAGAAAGCTGATTTAAAGAA 2636
QY 801 CysAsnIleValIleArgTyrGlyLeuValIleAsnGlnIleAlaMetValGlnAlaArg 820
Db 2637 TGTAACTATGTTATCCGTTATGCTGTCGTCAACCAATGAATAGCATGTGCCAGGCCGT 2696
QY 821 GlyArgAlaArgAlaAspGluSerThrTyrValLeuValAlaHisSerGlySerGlyVal 840
Db 2697 GGTGAGCCAGAGCTGATAGAGCACTACGCTGCTGTCACAGTGGTTCAGGAAGTT 2756
QY 841 IleGluHisGluThrValAsnAspPheArgGluLysMetMetTyrLysAlaIleHisCys 860
Db 2757 ATCGAACGTGAGCAAGTATATGATTTCCAGAGAAAGATATGATTAACCTATACATTGT 2816
QY 861 ValGlnAsnMetLysProGluGluTyrAlaHisLysIleLeuGluLeuGlnMetGlnSer 880
Db 2817 GTTCABAATATGAACCAAGAGATATGCTCATTAAGATTTTGGAAATTAACATGCAAGT 2876
QY 881 IleMetGluLysLysMetLysThrLysArgAsnIleAlaLysHisTyrLysAsnAsnPro 900
Db 2877 ATATGGAAGAAAGAAATGAAAAACAAGAAATATATCCAGAGACTTAACAAATTAACCA 2936
QY 901 SerLeuIleThrPheLeuCysLysAsnCysSerValLeuAlaCysSerGlyGluAspIle 920
Db 2937 TCACTATATACCTTCTTGCAAAAACGCAAGTGTCTAGCTGTGTGGGAAAGATATC 2996
QY 921 HisValIleGluLysMetHisHisValAsnMetThrProGluPheLysGluLeuTyrIle 940
Db 2997 CATTGATTTGAGAAATGATCATCGTCATATGACCCAGAAATTCAGGAATCTTACATT 3056
QY 941 ValArgGluAsnLysAlaLeuGlnLysLysCysAlaAspTyrGlnIleAsnGlyGluIle 960
Db 3057 GTAAAGAAAAACAAGCACTGCAAAAGAAAGTGGCCGACTATCAATAATATGCTGAATC 3116
QY 961 IleCysLysCysGlyGlnAlaTyrGlyThrMetMetValHisLysGlyLeuAspLeuPro 980
Db 3117 ATCTGAAATATGTCGCAAGGCTTGGGAAACAATGATGTGCACAAAGGCTTAATGATTTGCC 3176
|||||

QY 981 CysLeuIleValIleArgAsnPhenValValIlePheIysAsnAsnSerThrIlyIysGlnTyr 1000
 DB 3177 TGCTCAAAATAGGAATTTTGTAGTGGTTTCAAAAATATATTCACAAAGAAACATAC 3236
 QY 1001 LysIleTyrValGluLeuProIleThrPheProAsnLeuAspTyrSerGluCysCysLeu 1020
 DB 3237 AAAAAGTGGGTAAATTACTATCACATTTCCCAATCTTCACTATTCAGAAATGCTGTATA 3296
 QY 1021 PheSerAspGluAsp 1025
 DB 3297 TTTAGTATGATGAGAT 3311
 RESULT 11
 ADN04879
 ID ADN04879 standard; cDNA; 3379 BP.
 AC ADN04879;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Antipsoriatic cDNA sequence #654.
 XX
 KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX
 OS Homo sapiens.
 XX MO2004028479-A2.
 PN 08-APR-2004.
 PD 25-SEP-2003; 2003MO-US030907.
 PF 25-SEP-2002; 2002US-0414006P.
 PR (GETH) GENENTECH INC.
 XX
 PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;
 PI Wu TD;
 XX
 DR MPI; 2004-305105/28.
 DR P-PSDB; ADN04880.
 XX
 PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 PS Claim 1; SEQ ID NO 1273; 3069bp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polynucleotides of the invention.
 XX
 SO Sequence 3379 BP; 1152 A; 644 C; 753 G; 830 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3379
 Score: 5283.00 Matches: 1024
 Percent Similarity: 99.9% Conservative: 0
 Best Local Similarity: 99.9% Mismatches: 1
 Query Match: 99.5% Indels: 1
 DB: 12 Gaps: 0
 US-09-515-363c-2 (1-1025) x ADN04879 (1-3379)
 QY 1 MeSerAsnGlyTyrSerThrAspGluAsnPheArgTyrIleSerCysPheArgAla 20
 DB 169 ATGTGCAATGGATTCACAGACAGAAATTCGGCTATCTCATCTCGTCTCAGGACC 228
 QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40

DB 229 AGGGTAAAAATGATACATCCAGGTGAGCCTGTGCTGAGCTACCTGCTTCCTGCA 288
 QY 41 GluValIleValGlnIleGlnIleProThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
 DB 289 GAGGTGAAGAGAGATTCAGAGACAGTGGCAGCTCCGGGAAACATGCAAGGAGTTGAA 348
 QY 61 LeuLeuLeuSerThrLeuGluIlysgIlyValTyrPheIleGluIlyTyrThrArgIlePheVal 80
 DB 349 CTGCTGCTAGACACTTGGAGAAAGGAGTCTGGACACTTGTTGGACTCGGGAAATTCGAG 408
 QY 81 GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
 DB 409 GAGGCCCTCCGAGAACCCGACAGCCCTCGGGCCGCCCTGACATGAAACCTGAGCTCAG 468
 QY 101 AspLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeu 120
 DB 469 GACTGCTCTTCATCGTTTGAAGAGCTCAAGATGAATATCTCAACATGCTGAACCTC 528
 QY 121 LeuGlnProThrLeuValAspIysLeuLeuValArgAspValIleuAspIysCysMetGlu 140
 DB 529 CTTCAAGCCCACTCTGGTGAACAAGCTTCTAGTTAGAGACGCTTGATTAAGTCATGGAG 588
 QY 141 GluGluLeuLeuThrTleGluAspArgAsnArgIleAlaAlaAlaGluAsnAsnGlnIle 160
 DB 589 GAGGAATGTTGCAATTCAGAACAGAAACCGGATTCGCTGACAGAAACAAATGGAAT 648
 QY 161 GluSerGlyValArgGluLeuLeuIlysaArgIleValGlnIlysgIluAsnTrpPheSerAla 180
 DB 649 GAATCAGGTGTAAAGAGCTACTAAAGATTTGTGCAGAAAGAAACCTGGTCTTGCA 708
 QY 181 PheLeuAsnValIleuArgGlnThrArgIlysaAsnGlnIleuValGlnIlysgIlyser 200
 DB 709 TTTTGAATGTTCTTCTGCAACAGGAACAAATGAACCTTGCAAGTTAACAGGCTCT 768
 QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220
 DB 769 GATTGCTCAGAAAGCAATCAGATGAGATTTATCAACAAGTTGATGCTCTCAAGAG 828
 QY 221 GluGluGlnLeuLeuSerThrThrValGlnProAsnLeuGluIlysgIlyValTyrGlyMet 240
 DB 829 GAAGAGCAACTTCTTTCACCAACAGTTCAGCCAAATCTGAGAGAGAGGTCTGGGGCAG 888
 QY 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValIleSerGluSerAspThr 260
 DB 889 GAGAAATATCATCAGAAATCATCTTTTGCAGATCTCTTGATTTCAAGATTCAGACACA 948
 QY 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
 DB 949 AGTTTGGCAGAGAGAGTGTCAAGCTGCTTAGATGAAGCTTGACATTAACAGCAATG 1008
 QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
 DB 1009 GCGAGGATTCAGGACCCATGGAGATGATTCAGATGAAGAGAAATGTCAGCAAGACA 1068
 QY 301 SerProGluProGluLeuGlnIleuArgProTyrGlnMetGluValAlaGlnProAlaLeu 320
 DB 1069 TCCCGGAGACCAATCCAGCTCAGGCTTACCAATGGAAGTCCCAAGCAGGCTTGG 1128
 QY 321 GluGlyIlysaAsnIleIleIleCysLeuProThrGlySerGlyIlysaThrArgValAlaVal 340
 DB 1129 GAAGGAAATAATATCATCTGCTCCCTCAAGGAGAGTGGAAAAACAGAGTGGCTGTT 1188
 QY 341 TyrIleAlaIlysaAspHisLeuAspIlysaIlysaIlysaIlysaIlysaIlysaIlysa 360
 DB 1189 TACATTGCCAAGATCATTTAGACAAAGAAAGAAAGAAAGCAATGAGCTGAGAAAGTTATA 1248
 QY 361 ValIleuValAsnIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysa 380
 DB 1249 GTTCTTGTCAATTAAGTATCTGCTAGTTGAACAGCTCTTCGCAAGAGATTCACCAATTT 1308
 QY 381 LeuIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysa 400
 DB 1309 TTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368

QY	401	ProGluValValLysSerCysAspIleIleIleSerThrAlaGlnIleLeuGluAsnSer	420
Db	1369	CSAGAGGTGTCAGAGTCTGTGATATATATATATATGAGTCAAGTCAAACTCTGAAATCTCC	1428
QY	421	LeuIleAsnLeuGluAsnGluGluAspAlaGlyAlaGluLeuSerAspPheSerLeuIle	440
Db	1429	CTCTTAACTTGGAAGAAATGGAGAGAGTGTGTCTGATTCAGATCTGACATTTTCCCTCAAT	1488
QY	441	IleIleAspGluCysGlnHisIleThrAsnIleGluAlaValTyraAsnIleMetArgHis	460
Db	1489	ATCATGATGATGATGATGATCATCAGCAGCAAG - GAGGAGGTATTAATTAATCATGAGGAT	1547
QY	461	TyrLeuMetGlnLysLeuLysValAsnAsnArgLeuLysLysGluAsnLysProValIlePro	480
Db	1548	TATTTGATGACGAGAGGTTGAAAAACATAGACTCAAGAAAGAAAAACAAACAGTATTTCC	1607
QY	481	LeuProGlnIleLeuGluLysLeuThrAlaSerProGlyValGlyValAlaThrLysGluAla	500
Db	1608	CTTCTCGATGATCTGGGACTAAGCTTCAAGCTTGGTGTGGAGGGGCCAGAGCAAGCC	1667
QY	501	LysAlaGluGluHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThrIleLysThr	520
Db	1668	AAAGGTGAAGAACATTTTAAACTATAGTGCATCTGATGATTTACTATTAAACT	1727
QY	521	ValLysGluAsnLeuAspGlnLeuLysAsnGlnIleGlnGluProCysLysLysPheAla	540
Db	1728	GTTAAAGAAAACTTTGATCAACTGAAAAACAAATACAGGAGCCATGCAAGAAATTTGCC	1787
QY	541	IleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeuGlnIleMetThrArg	560
Db	1788	ATTGAGATGCAACAGAGAAAGATCATTTAAAGAAACTTCTAGAAATATATACAGG	1847
QY	561	IleGlnThrTyrcysGlnMetSerProMetSerAspPheGluThrGlnProTyrcGluGln	580
Db	1848	ATTCAAACTTATTTGTCAATGATGTCATATGTCAGATTTTGGAACTCAACCTTAGAACAA	1907
QY	581	TrpAlaIleGlnMetGlnLysLysAlaAlaLysLysGluAsnArgLysGluArgValCys	600
Db	1908	TGGGCGCATTCAAATGGAAAAAAACCTCCAAAAAGAAAAATCGCAAGAAACGTTTGT	1967
QY	601	AlaGlnHisLeuArgLysTyraAsnGluAlaLeuGlnIleAsnAspThrIleArgMetIle	620
Db	1968	GCGAGACATTTGAGAGAGTACATAGAGCCCTTCAAAATTATGACACAACTTGGATGATA	2027
QY	621	AspAlaTyrrHisIleLeuGluThrPheTyraAsnGluLysAspLysLysPheAlaVal	640
Db	2028	GATGCGTATACATCATCTTGAAACTTTCTATATATAGAAAGAAAGATATAGAACTTGCAGTC	2087
QY	641	IleGluAspAspSerAspGluGluLysLysAspArguTyrcysAspGluAspGluAspGlu	660
Db	2088	ATAGAGAGATGATAGATAGAGGGGTGTATGTATGTATGTATGTATGTATGTATGTATGTAT	2147
QY	661	AspAspLeuLysLysProLeuLysLeuAspGluThrAspArgPheLeuMetThrLeuPhe	680
Db	2148	GATGATTTTAAAGAAACTTTTGAACTGGATGAAACAGATAGATTTCTCATGACTTTATTT	2207
QY	681	PheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnProGluTyrcGluAsnGluLys	700
Db	2208	TTTGAACAAATTAATATGTTGAAAGAGCTGCTGTGAAAAACCAAGATATAGAAAAAGAAAG	2267
QY	701	LeuThrLysLysLeuArgAsnThrIleMetGluGlnIleTyrrArgThrGluLysSerAlaArg	720
Db	2268	CTGACCAAAATTAAGAAATACCAATATGAGCAATATCTAGAGACTGAGAGAAATCAGACGA	2327
QY	721	GlyIleIlePheThrLysThrArgLysSerAlaTyrrAlaLeuSerGlnTrpIleThrGlu	740
Db	2328	GGAATATATCTTTTACAAAAACAGACAGAGTGAATGGCGCTTTCCCATGATGATTACTGAA	2387
QY	741	AsnGluLysPheAlaGluValGlyValLysAlaHisIleLysLeuIleGlyValGlyHisSer	760
Db	2388	AATGAAAAAATTTGCTGAGTAGAGATGCAAAAGCCCAATCTGATTTGGAGCTGACACAGC	2447

QY	761	SetrluphelvSPrometThnglnaenGluGlnlysglValIieserLySPheArgThr	780
Db	2448	AGTAGTTCAAACCCATGACACAGAAAGAACAAAAGAGTCACTAGTAATTTCCGACT	2507
QY	781	GlyLySIIleAnLeuLeuIleAlaThrThrValaIagluGluGlyLeuAspIleLySglu	800
Db	2508	GGAAAAATCAATCTGCTTATTCGTACACAGTGGCAGAGAGGTCTGATATTAAAGAA	2567
QY	801	CysAenIIleValIIleArgTYrGlyLeuValIThrAnGluIleAlaMetValGlnAlaArg	820
Db	2568	TGTAAACATTGTTCATCCGTATGTGCTGTGCATCCATATAATAGCAATGTCAGGCCGT	2637
QY	821	GlyArGAlaArgAlaAspGluSerThrTYrValLeuValaIAsnIserGlySerGlyVal	840
Db	2638	GGTCAGCCAGAGCTGATAGAGACACTAGCTCTGTTGCTCAAGTGGTTCAGAGTT	2687
QY	841	IIleGluHISgluThrValaAsnAspPheArgGluLySmetCetyLyAlaIleHIScys	860
Db	2688	ATCGAACATGAGACAGTTAATGATTCGAGAGAGAGATGATGTATAAGCATATCATTTGT	2747
QY	861	ValGlnAenMetLySProGluGluTYrAlaHISLySIIleGluGluLeuGlnMetGlnSer	880
Db	2748	GTTCAAAATATAGAAACAGAGAGATAGCTCATAGATTTTGGAAATTCAGATGCCAAAGT	2807
QY	881	IIleMetGluLyLySmetLySThrLyArgAsnIIleAlaLySHSTyrlLyAsnAsnPro	900
Db	2808	ATAATGAGAAAGAAATGAAAAACAGAGAAATTTCTCCAGACATTCACAGAAATACCCA	2867
QY	901	SerLeuIleThrPheLeuCyLySAsnCySerValIleuAlaCySerGlyGluAspIle	920
Db	2868	TCACTAATTAATCTTCTCTTGCAAAAATCGCAGTGTCTAGCTGTTCTGGGGAAGATATC	2927
QY	921	HISValIIleGluLySmetHISHisValaAsnMetThrProGluPheLySgluLeuTYrIle	940
Db	2928	CATGTAATTGAGAAATGCAATCATCGTCATATGTAGACCCAGAAATTCAGGAACTTACATT	2987
QY	941	ValArGgluAenLySIIleLeuGlnLyLySValaAspTYrGlnIIleAnGluGluIle	960
Db	2988	GTAAGAGAAACAAAGCATGCAACAAAGAGTGTCCGACTATCAATTAATATGGTGAATC	3047
QY	961	IIleCyLySVCySglYglnAlaTYrGlyTYrHISmetCValIHISLySglYLeuAspLeuPro	980
Db	3048	ATCTGCCAATGTGGCCAGGCTTGGGGAAACATATGATGTGCACAAAGCTTAGATTTCCT	3107
QY	981	CysLeuLySIIleArgAsnPheValaValaPheLySAsnAsnSerThrLyLySgluTYr	1000
Db	3108	TGTCTCAAAATAGGAATTTTGTAGTGGTTTCCAAAATATATTCAAACAAAGAAACAATAC	3167
QY	1001	LySlySTPValIIGluLeuProIIleThrPheProAenIleuAspTYrSerGluCySValLeu	1020
Db	3168	AAAAAGTGGTGAATTCATTCATCAATTTCCAAATCTGACTATTCAGAAATGCTGTATTA	3227
QY	1021	PheSerAspGluAsp 1025	
Db	3228	TTTAGTGATGAGGAT 3242	
RESULT 12			
AAD11170			
ID AAD11170 standard; DNA; 3131 BP.			
AAC AAD11170;			
XX			
DT 29-NOV-2001 (first entry)			
DE Human melanoma differentiation associated-5 protein-related DNA.			
XX			
KW Human melanoma differentiation associated gene; Mda-5; interferon; IFN;			
KW RNA helicase motif; caspase recruitment domain; CARD; therapy; melanoma;			
KW neuroblastoma; astrocytoma; glioblastoma; multiforme; cancer; cervical;			
KW breast; colon; prostate; osteosarcoma; chondrosarcoma; systemic toxicity;			
KW central nervous system; cytostatic; apoptosis; ds.			
XX			
OS Homo sapiens.			

XX MO200164707-A1.
 PN 07-SEP-2001.
 XX 28-FEB-2001; 2001MO-US006960.
 XX 29-FEB-2000; 2000US-00515363.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX Fisher PB, Kang D, Gopalakrishnan RV,
 XX WPI; 2001-565494/63.
 DR Nucleic acid sequences encoding a Melanoma Differentiation Associated
 PT Gene useful for cancer cell growth suppression, apoptosis and anti-viral
 PT activity.
 XX
 PS Disclosure; Page 134-148; 152pp; English.
 XX
 CC The present invention relates to an isolated nucleic acid encoding a
 CC melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5
 CC contains a caspase recruitment domain (CARD) and a RNA helicase motif.
 CC Mda-5 is a novel interferon (IFN) inducible gene with structural
 CC similarities to RNA helicases and CARD motif containing proteins. Mda-5
 CC is induced during terminal differentiation in human melanoma cells
 CC treated with the combination of recombinant fibroblast IFN and the
 CC anti-leukemic compound mezerein (Mez). Mda-5 is useful for identifying
 CC compounds that may induce its expression. Mda-5 is useful for treating
 CC cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma
 CC multifome, cervical cancer, breast cancer, colon cancer, prostate
 CC cancer, osteosarcoma, chondrosarcoma and especially where the cancer is a
 CC cancer of the central nervous system and apoptosis. The Mda-5 promoter
 CC exhibits melanocyte tissue specificity and minimises systemic toxicity.
 CC The present sequence is designated SEQ ID NO:2 in the sequence listing, but
 CC does not correspond to the sequence designated SEQ ID NO:2 in the main
 CC body of the specification (AAE10155). The present sequence is not further
 CC referred to in the specification, and has been represented in a protein
 CC format in the sequence listing
 CC
 XX
 SQ Sequence 3131 BP; 1075 A; 583 C; 699 G; 774 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3131
 Score: 5276.50 Matches: 1024
 Percent Similarity: 99.7% Conservative: 0
 Best Local Similarity: 99.7% Mismatches: 0
 Query Match: 99.4% Indels: 3
 DB: 4 Gaps: 1
 US-09-515-363c-2 (1-1025) x AAD11170 (1-3131)
 QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20
 DB 1 ATGTCCAAATGGATATTCACAGACGAGAAATTTCCGCTATCTTCGTGCTTCAAGGCC 60
 QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
 DB 61 AGGGTGAATAATGATCAATCCAGGTGAGCTGTGCTGACCTGACCTTTCGCGCTGCA 120
 QY 41 GlnValIleGlnGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
 DB 121 GAGGTAAAGAGAGACATTCAGAGACAGTGCACCTCCGGGAAACATGCGAGCATTTGAA 180
 QY 61 LeuLeuLeuSerThrLeuGlnIleGlnValIleTyrIleGlnGlnTyrThrArgGlnPheVal 80
 DB 181 CTCCTGCTGACACCTTGGAGAAAGAGCTGTGGCACTTGTGACTCGGGAATTCGTG 240
 QY 81 GlnAlaLeuArgArgThrGlnIleSerProLeuAlaAlaArgTyrMetAsnProGlnLeuThr 100
 DB 241 GAGGCCCTCCGGAGAACCGGCAAGCCCTCTGCGCGCCGCTACATGAACCTGTGAGTCAAG 300

QY 101 AspLeuProSerProSerPheGluAsnAlaIleAspGluTyrLeuGlnLeuLeuAsnLeu 120
 DB 301 GACTTGCCCTCTCAATCGTTTGAGAACGCTCAAGATGATATCTCCAACTGCTGAACCTC 360
 QY 121 LeuGlnProThrLeuValAspIleLeuLeuValArgAspValIleuAspIleCysMetGlu 140
 DB 361 CTCACGCCCACTGTGTGAGCAAGCTTCTAGTTAGAGACGCTTGTGATAGTCAATGAG 420
 QY 141 GlnGlnLeuLeuThrIleGlnAspArgAsnArgIleAlaAlaIleGlnAsnGlnIleAsn 160
 DB 421 GAGAACTGTTCACATTTGACAGAAACCGGATTTGCTGTCAGAAAAACATGTGAAT 480
 QY 161 GluSerGlyValArgGlnLeuLeuIleValGlnIleGlnIleGlnIleGlnIleGlnIle 180
 DB 481 GAATCAGGTGTAGAGAGCTACTTAAAGATTTGTGAGAAAGAAATCTGTTCTCTGCA 540
 QY 181 PheLeuAsnValIleuArgGlnThrGlyAsnAsnGlnLeuValGlnGlnLeuThrGlnIle 200
 DB 541 TTTCTGAATGTTCTTCTGTCMAACAGAAACATGAATGAACTTGTCCAAAGTTAACAGGCT 600
 QY 201 AspCysSerGlnSerAsnAlaGlnIleGlnAsnLeuSerGlnValAspGlyProGlnVal 220
 DB 601 GATTGCTCAGAAAGCAATGACAGATTGAGAAATTTATCACAGTTGATGCTCTCAAGT 660
 QY 221 GlnGlnGlnLeuLeuSerThrThrValGlnProAsnLeuGlnIleGlnIleGlnIleGln 240
 DB 661 GAGAGCAACTTTTTCACACACAGTTCCAGCAAACTTGAGAGAGAGGTCTGGGCGATG 720
 QY 241 GluAsnAsnSerSerGlnSerPheAlaAspSerSerValIleSerGlnSerAspThr 260
 DB 721 GAGAAATACATCATCAATCATCTTTTGGAGATTCTTCTGTAGTTACAGATCAGACACA 780
 QY 261 SerLeuAlaGlnGlnIleSerValSerCysLeuAspGlnSerLeuGlnIleIleAsnSerAsnMet 280
 DB 781 AGTTTGCGAGAGAGAGTGCACCTCTTAGAGAAAGCTTGGACATTAACACCAACATG 840
 QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGlnGlnAsnValAlaAlaArgAla 300
 DB 841 GGCAGTGATTCAGGACCAATGGAGATGATTCAGATGAAAGATGTGGACGACAGACGA 900
 QY 301 SerProGlnProGlnLeuGlnLeuArgProTyrGlnMetGlnValAlaGlnProAlaLeu 320
 DB 901 TCCCGGAGGACAGAAATCCACAGCTCAGCGCTTACCAATGGAAGTTCCCGACGACCTTG 960
 QY 321 GlnGlnIleValAsnIleIleIleCysLeuProThrGlnIleSerGlyIleThrArgValAlaVal 340
 DB 961 GAAGGAGAAATATCATCATCTGCTCCCTACAGGAGTGAGAAAAACCAAGATGCGCTGT 1020
 QY 341 TyrIleAlaIleValAspIleLeuAspIleValIleValIleValIleValIleValIle 360
 DB 1021 TACATTGCGAAGATATCATTTAGACAAAGAAAGAAAGAAAGCAATCTGAGCGTGAAGAAATTA 1080
 QY 361 ValLeuValAlaAsnValIleLeuLeuValGlnGlnLeuPheArgIleGlnPheGlnProPhe 380
 DB 1081 GTTCTTGTCAATAGGATCTGCTAGTTGAACGCTCTTCCGCAAGAGATTTCCAAACATTT 1140
 QY 381 LeuIleValSerTyrTyrArgValIleGlyLeuSerGlyAspThrGlnLeuIleIleSerPhe 400
 DB 1141 TTGAAGAAATGATGATGTGATTTAGGATTAAGTGATGATACCAATCGAAAAATATCATTT 1200
 QY 401 ProGlnValValIleSerCysAspIleIleIleSerThrAlaGlnIleLeuGlnIleAsnSer 420
 DB 1201 CCAGAAATGTTCAGATCTGTGAT--ATTATCAGTACAGCTCAATATCTTGAAAACTCC 1260
 QY 421 LeuLeuAsnLeuGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 440
 DB 1258 CTCCTTAACCTTGGAAAAATGAGAGAGATGCTGCTTCAATTTGACACTTTTCCCTCAT 1317
 QY 441 IleIleAspGlnCysIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 460
 DB 1318 ATCATTTGATGAATGATCATCAACCAACAAAGAGAGTGTATTAATTAATCATGAGGCAAT 1377

QY 461 TTTLeuMetGluLeuLeuYsaAenAenrgLeuLeuYsgLueuLeuYsProValIlePro 480
 Db 1378 TATTTATGACAGAAAGTTGAAAAACAATAGACTCAAGAAAGAAAAACAACAGAGATTCCC 1437
 QY 481 LeuProGlnIleLeuGluLeuThrAlaSerProGluValGluGluValThrIleYsgIleAla 500
 Db 1438 CTTCCTCAAGATACCTGGACCTAACAGCTTCACCTGGGTGGAGGGGCGACGAAGCAAGCC 1497
 QY 501 LysAlaGluGluIleLeuLeuYsLeuCyAlaAenLeuAenAlaPheThrIleYsThr 520
 Db 1498 AAAAGCTGAAGAACACATTTTAAACTATGTGCCAATCTTGATGCACTTACTATTAAGCT 1557
 QY 521 ValIleYsgLeuAenLeuAenProGluLeuYsAenGlnIleGlnGluProCyLeuYsPheAla 540
 Db 1558 GTTAAAGAAAACTTGATCACTGAAAAACAATACAGAGGCCATGCAAGAGTTGGCC 1617
 QY 541 IleAlaAenAlaThrArgGluAenProPheYsgIleLeuLeuGlnIleMetThrArg 560
 Db 1618 ATTGCAGATGCACACAGAAAGATCCATTTAAAGAGAACTTGTAGAAATATGACAAAG 1677
 QY 561 IleGlnThrTyrcyGlnMetSerPrometSerAspPheGluYThrGlnProTyrgLugln 580
 Db 1678 ATTCAAACTTATTTGCAATAGATCCAAATGTCAGATTTTGGAACTCAACCTTATGAACAA 1737
 QY 581 TTPAlaIleGlnMetGluYsgValAlaIleYsgIleYsaAenrgIleYsgIleArgValCys 600
 Db 1738 TGGGCATTCCAATGGAAAAAAGCTGCAAAAAAGAAATCGCAAAAGACGTGTTGT 1797
 QY 601 AlaGluIleLeuAenrgYsTyraenGluAlaLeuGlnIleAenPheThrIleAenMetIle 620
 Db 1798 GCGAAACATTTGGAGAAATGCAATGAGGCCCTCAATTAATATACCAATTCCAATGATA 1857
 QY 621 Asp--AlaTyThrIleLeuGluThrPheTyraenGluGluYsAspIleYsPheAlaVal 640
 Db 1858 GATCCCGCTATCTCATCTTGAACCTTTCTATATAGAGAAAGATTAACAAGCTTGGCAG 1917
 QY 640 aIIleGluAenAenSerAspGluGluYsaAenPheGluTyrcyAenrgIleYsPheGluAenrg 660
 Db 1918 TCATAGAAAGATGATGATGATGAGGGTGGTGTGATGATGATGATGATGATGATGATGATG 1977
 QY 660 LysAenPheLeuYsYsProLeuLeuLeuAenrgIleThrAenPhePheLeuMetThrLeuP 680
 Db 1978 AGGATGATTTTAAAGAAACCTTTGAAACCTGATGAAACAGATTAATTTCTATATCACTTAT 2037
 QY 680 hePheGluAenAenYsMetLeuYsArgLeuAlaGluAenProGluTyrcyGluAenrgIle 700
 Db 2038 TTTTGAACCAATTAATTAATTTGAAAGCTGCTGCTGAAAAACCAAGATATGAAATGAAA 2097
 QY 700 YsLeuThrIleYsLeuAenrgAenThrIleMetGluGlnTyrcyThrArgThrGluGluSerAla 720
 Db 2098 AGCTGACCAAAATTAAGAAATACCATATGAGCAATATCTAGAGCTGAGAGATCAGCAC 2157
 QY 720 rgGluIleIlePheThrIleYsThrArgGlnSerAlaTyrcyAlaLeuSerGlnThrIlePheArg 740
 Db 2158 GAGGAATTAATCTTTACAAAAACAGACAGATGATATGGCTTTCCCACTGAGATTAATCG 2217
 QY 740 LysenGluYsPheAlaGluValGluValYsaIleYsIleYsIleGluValAlaGluYhis 760
 Db 2218 AAAATGAAAAATTTGCTGAAGTGAAGTCAAAAGCCCACTGATGATGAGCTGAGACACA 2277
 QY 760 eysGergluPheYsProMetThrGlnAenGluGlnYsgIleValIleSerIlePheArgT 780
 Db 2278 GCAGTGAGTTCAAAACCATGACACAGAAATGAACAAAAGAAAGCATTAATAATTTGCGA 2337
 QY 780 hrgIleYsIleAenLeuLeuIleAlaThrThrValAlaGluGluGluYsLeuAenrgIleYsg 800
 Db 2338 CTGGAATAATCAATGCTTATGCTTACCAAGGCGAGAAAGGCTGAGATATTAAAG 2397
 QY 800 lueCyAenIleValIleArgTyrcyLeuValIleThrAenGluIleAlaMetValGlnAla 820
 Db 2398 AATGTAACTTTTATTCGTTATGCTGCTGCTGCAACCAATGAATGCAATGCTCAAGGCC 2457
 QY 820 rgGluYrgAlaArgAlaAenrgIleSerThrTyrcyValleuValAlaIleSerGluYsGlu 840

Db 2458 GTGGTCGACCCAGAGCTGATGAGACACTACGTCCTGGTCTCAACAGTGTTCAGAG 2517
 QY 840 aIIleGluIleGluThrValIleAenPheAenrgIleYsMetMetTyrcyValAlaIleIleAC 860
 Db 2518 TTATCGAACATGAGACAGTAAATGATTTCCGAGAAAGATGATGATTAAGCTATACAT 2577
 QY 860 YsValGlnAenMetYsProGluGluTyrcyAlaIleYsIleLeuGluLeuGlnMetGlns 880
 Db 2578 GTGTTCAAAATATGAAACAGAGAGATATGCTCATATGATTTTGGAAATTAACAGATGC 2637
 QY 880 eIIleMetGluYsYsMetYsThrIleYsAenIleAlaYsIleTyrcyIleYsAenAenrg 900
 Db 2638 GTATATATGAAAAAGAAATGAAAAACCAAGAAATATTTGCCAAGCATTAACAAGATTAAC 2697
 QY 900 roSerLeuIleThrPheLeuCyLeYsAenCySerValIleuAlaCySerGluYsgIleAenrgI 920
 Db 2698 CATCACTAATTAATCTTCTTCCGAAAACTGCAAGTGTGCTTACCTGTTCTGGGGAAAGAT 2757
 QY 920 leIleValIleGluYsMetIleYsValIleAenMetThrProGluPheYsgIleLeuTyrcy 940
 Db 2758 TCCATGTATTTGAGAAATGATCATCAGTCAATATGACCCCAAGAAATTCAGAGAACTTTACA 2817
 QY 940 leValIleGluLeuLeuYsAlaLeuGlnIleYsLeuCyAenIleAenrgIleAenrgIle 960
 Db 2818 TTGTAAAGAAAAACAAGACATGCAAAAGAGGTGCCATATATCAATTAATTAATGAGTGA 2877
 QY 960 leIleCyYsCyGluGlnAlaATPGLuYThrMetMetValIleYsGluYsLeuAenrgIle 980
 Db 2878 TCATTCGAAATGTGGCCAGGCTTGGGGAACAATATGATGATGCAAAAGCTTATGATTCG 2937
 QY 980 roCyLeuLeuYsIleAenPheValIleValIleYsAenAenSerThrIleYsGlnIle 1000
 Db 2938 CTGTCTCAAAATTAAGAAATTTGTATGTGTTTCAAAATTAATTCMAAGAAACAAT 2997
 QY 1000 YrcyIleYsThrValGluLeuAenrgIleThrPheProAenLeuAenrgIleYsGluCyAenrg 1020
 Db 2998 ACAAAAGGTGGAGTAATTAATCATCATATTCCTCAATCTTGAATTCAGAAATGCTGTT 3057
 QY 1020 eupheSerAenrgIleAenrg 1025
 Db 3058 TATTTAGTATGAGGAT 3074
 Db 3058 TATTTAGTATGAGGAT 3074
 RESULT 13
 ADQ22237
 ID ADQ22237 standard; DNA; 3668 BP.
 AC ADQ22237.
 XX
 DT 26-AUG-2004 (first entry)
 XX
 XX
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5057.
 XX
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW de.
 OS Homo sapiens.
 XX
 XX
 PN W02004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 XX 26-NOV-2003; 2003MO-US038193.
 PF
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Aziz N, Ginsburg WM, Zlotnik A;
 PI
 XX
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX Example 2; SEQ ID NO 5057; 210bp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 3668 BP; 1215 A; 730 C; 811 G; 872 T; 0 U; 40 Other;

Alignment Scores:

Pred. No.: 0 Length: 3668
Score: 5251.00 Matches: 1015
Percent Similarity: 99.1% Conservative: 1
Best Local Similarity: 99.0% Mismatches: 9
Query Match: 98.9% Indels: 0
DB: 12 Gaps: 0

US-09-515-363C-2 (1-1025) x ADQ22237 (1-3668)

QY 1 MetSerAsnGlyTyrTerSerThrAspGluAsnPhenArgTyrLeuLysSerCysPheArgAla 20
DB 169 ATGTCAAAATGGGATTTCACACGACGAAATTCGGTATCTCATCTCGTTCAGAGGCC 228
QY 21 ArgValIleMetCytTrlIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
DB 229 AAGGTGAAAATGTACATCCAGGTGGAGCCTGTCTGTGACTGACTGACCTTTCTGCTCGA 288
QY 41 GluValIleGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 289 GAGGTGAAGAGAGATTCAAGAGACATGCGCACCTCCGGGAAATGACGAGATTGAA 348
QY 61 LeuLeuLeuSerThrLeuGlnIlyGlyValTrrPheLeuGlyTrrPheArgGluPheVal 80
DB 349 CTGCTGCTAGACCTTGGAGAGAGCTGGCACCTTGTTGGACTCGGGAAATTCGTG 408
QY 81 GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
DB 409 GAGGCCCTCCGAGAACCGGACCCCTTGGCCGCCCTACATGAACTTGAGCTCAG 468
QY 101 AspLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeu 120
DB 469 GACTGGCCCTCCCATCGTTTGAGAACGCTCATGAGATATCTCCAACTGCTGAACCTC 528
QY 121 LeuGlnProThrLeuValAspIlyLeuLeuValArgAspValIleuAspIlyCysMetGlu 140
DB 529 CTTTCAGCCCACTCTGGTGGACAAGCTTCTAGTTAGACGCTCTTGATTAAGTCCATGGAG 588
QY 141 GluGluLeuLeuThrTrlIleGluAspArgAsnArgTrlAlaAlaIleGluAsnAsnGluYaa 160
DB 589 GAGGAACGTGTGACATTTGAGACAGAAACCGATTGCTGCAAGAAACATAGGAAT 648
QY 161 GluSerGlyValArgGluLeuLeuLysArgIleValGlnLysGluAsnTrpPheSerAla 180
DB 649 GATCAGGTGTAGAGAGGACTATAAAAGATTGTGCAAGAAAGAAACCTGCTCTGCA 708
QY 181 PheLeuAsnValIleuArgGlnThrTrlYAsnAsnGluLeuValGlnGluLeuThrGlySer 200
DB 709 TTTTGAATGNNNNNNNNNNNNNNNNNNNNATGAACCTGTCCAAAGATTAAACAGGCTCT 768
QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220

DB 769 GATTGCTCAGAAAGCAATCAGAGATTGAGAAATTTATCACAAGTTGATGCTCTCAAGTG 828
QY 221 GluGluGlnLeuLeuSerThrThrValGlnProAsnLeuGluLysGluValTrrPglyMet 240
DB 829 GAAGAGCAACTCTTTCAACCAAGTCCAGCCAAATCTGAGAGAGAGGCTGGGGCAGTG 888
QY 241 GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValIleSerGluSerAspThr 260
DB 889 GAGAAATCACTATCAGAAATCATCTTTTGAGATTCTTCTGTAGTTCCAGATACAGACA 948
QY 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
DB 949 AGTTTGACAGAGAAAGTGTGAGCTGCTTAAAGTGAAGCTTGACATAAACGCAACATG 1008
QY 281 GlySerAspSerGlyTyrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
DB 1009 GGCAGGATTCAGGACCCATGGGAGTGAATTGAGTGAAGAGAAATGTGCAGACAGACA 1068
QY 301 SerProGluProGluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeu 320
DB 1069 TCCCGGAGCCAGAACTCCAGCTCAGGCTTACCAATATGAAGTTGCCAGCCAGCTTGG 1128
QY 321 GluGlyIlyAsnIleIleIleCysLeuProThrGlySerGlyIlySerThrArgValAlaVal 340
DB 1129 GAAGGAAAGAAATATCATCTATCTGCTCCCTACAGGAGTGAAGAAACCAAGAGTGGCT 1188
QY 341 TyrIleAlaIlyAspHisIleuAspIlyIlyIlyValIleSerGluProGlyIlyValIle 360
DB 1189 TACATTGCCAAGAGATCACTTACACAAAGAAAGAAATCTGAGCTGGAAGAAAGTTATA 1248
QY 361 ValIleuValAsnIlyValIleuLeuValGluGlnLeuPheArgGluPheGlnProPhe 380
DB 1249 GTTCTTGTCAATAGGTACTGCTAGTTGAACAGCTCTTCCGAGAGAGTTCCAAACATTT 1308
QY 381 LeuIlyIlySerTyrArgValIleGlyLeuSerGlyAspThrGlnLeuIlyIleSerPhe 400
DB 1309 TTGAAGAAATGGATATGCTGTATTGATTAAAGTGGATACCAATGAAATATCATATT 1368
QY 401 ProGluValIlyIlySerCysAspIleIleIleSerThrAlaGlnIleuGluAsnSer 420
DB 1369 CCAGAAATGTCAAGCTGTATATTATACAGTACAGCTCAATCTTGAAACCTCC 1428
QY 421 LeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuIle 440
DB 1429 CTTTAACTTGAATAATGAGAAATGCTGTGTTCATTTGTCAACTTTTCCCTCATTT 1488
QY 441 IleIleAspGluCysHisIleThrAsnIlyGlnAlaValTyrAsnAsnIleMetArgHis 460
DB 1489 ATCATTTGATGATGTATCATACACCAACAAAGAGAGGTATATATACATCATGAGGCAT 1548
QY 461 TyrLeuMetGlnIlyLeuIlyAsnAsnArgLeuIlyIlyGluAsnIlyProValIlePro 480
DB 1549 TATTTGATCAGAAAGTTGAAAAACATATAGCTCAAGAAAGAAACCAACAGATGATCCC 1608
QY 481 LeuProGlnIleGluIlyLeuThrIleSerProGlyValGlyValAlaThrIlyGlnAla 500
DB 1609 CTTTCCAGATCTGGAGCTTAACGCTTCACTGGGTGGAGGGGCCAGAGCAAGCC 1668
QY 501 IlyAlaGluGluHisIleLeuIlyLeuCysAlaAsnLeuAspAlaPheThrIleIlyThr 520
DB 1669 AAGCTGAAAGAACATTTTAAACATATGTGCCAATCTTGAGTCATTTCTATTAAACCT 1728
QY 521 ValIlyGluAsnLeuAspGlnLeuIlyAsnGlnIleGlnGluProCysIlyIlyPheAla 540
DB 1729 GTTAAAGAAACCTTGATCACTGAAACCAAAATACAGAGCCATGCAAGAGATTGGCC 1788
QY 541 IleAlaAspAlaThrArgGluAspProPheIlyGluIlyLeuLeuGlnIlyIleMetThrArg 560
DB 1789 ATTGCAGATGCAACGAGAAATTCATTTAAAGAAACCTTCAAGAAATATGACAAAG 1848
QY 561 IleGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGluGln 580

Db 1849 ATTCAAACTTAATGTCMAAAGAGTCAGATCTCAGATTTTGGAACTCAACCTATGAACA 1908
 Qy 581 TTPAlaIleGIeMeGluLySylValaIaLyLeGIYaSnArghySgluArGValaCys 600
 Db 1909 TGGGCCATTCAATGGAAGAAAAAGCTGCAAAAAGAAATGCGAAAGAACCTGTTTGT 1968
 Qy 601 AAGLuHLeuArghySylrAengluAlaLeuGlnIleAsnArpThrIleArghyMetIle 620
 Db 1969 GCGAAGACATTTGAGGAAGTACATGAGGCCCTCAATTAATGACCAATTCGAATGAAATG 2028
 Qy 621 AAspAlaTyThrThiAlaLeuGluThrPheTyrrAengluGluLyAspLySylSylPheAlaVal 640
 Db 2029 GATGCGTAATACATCATCTTGAACCTTCTAATAAGAAAGAAATGAAGATTGGAAGTC 2088
 Qy 641 ILeGIAspAspSerAspGluGlyGIYaAspAspGluTyrrCysAspGlyAspGluAspGlu 660
 Db 2089 ATAGAAGATGATGATGATGAGGTGGTGTGATGATGATGATGATGATGATGATGATGATG 2148
 Qy 661 AspAspLeuLyLeuAspProLeuLyLeuAspGluThrAspArghPheLeuMetThrLeuPhe 680
 Db 2149 GATGATTTAAAGAAACCTTTGAAACCTGATGAAGAAACGATGATTTCTCATGACTTATTT 2208
 Qy 681 PheGluAsnAsnLySylMetLeuLySylValaLeuAlaGluAsnProGluTyrrGluAsnGluLyS 700
 Db 2269 CTGACCAAAATTAAAGAAATCCATTAATGAGACAAATATCTGAGCTGAGAACTGACACGA 2228
 Qy 721 GIYIleIlePheThrLySylrAengluInSerAlaTyrrAlaLeuSerGlnTrpIleThrGlu 740
 Db 2329 GGAATATCTTTCAAAAAACACACAGAGTCATATGCCCTTCCAGTGATTAATCTGA 2388
 Qy 741 AAspGluLyPhePheAlaGluValaGlyValaLySylAlaHisIleSylIleGlyAlaGlyHisSer 760
 Db 2389 AATGAAAAAATTTCTGTAAGTAGAGATCAAAAGCCACCATCTGATGAGCTGACACAGC 2448
 Qy 761 SerGluPheLySylProMetThrGluInAsnGluGluValaIleSerLySylPheArghThr 780
 Db 2449 AGTGAAGTTCAAAACCATGACACAGATGAAACAAAGAAATGCTAATTAATTTCCGACT 2508
 Qy 781 GIYLySylLeuAsnLeuSylAlaArhThrValaAlaGluGluGluAspIleLySylGlu 800
 Db 2509 GGAATAATTAATCTGCTTATCGCTACACAGTGGCAGAAAGATGCTGATATTAAAGAA 2568
 Qy 801 CysAsnIleValaIleArghTyrrGlyLeuValaThrAengluIleAlaMetValaGlnAlaArg 820
 Db 2569 TGTAAATGTTGTTATCCGTTATGCTGCTGTCACCAATGAATAGCATGATGCTCAGGCCGT 2628
 Qy 821 GLYArGIaArghIaAspGluSerThrTyrrValleuValaAlaHisSerGlySerGlyVala 840
 Db 2629 GGTGAGGCCAGAGCTGATGAGAGCACTTACGCTGCTGCTCACTGCTTCAAGAGTT 2688
 Qy 841 ILeGIuHLeuGluThrValaAsnArghPheArghLySylMetMetTyrrLySylAlaIleHisCys 860
 Db 2689 ATGGAACGTGAGACAGTATTAATGATTTCCGAGAGAAAGTATGATTAAGCTATACATGCT 2748
 Qy 861 ValGIaAsnMetLySylProGluGluTyrrAlaHisLySylIleLeuGluLeuGlnMetGlnSer 880
 Db 2749 GTTCAAAATATGAAACAGAGAGATGATCTCATTAAGATTTTGGAAATTAAGATGCAAGT 2808
 Qy 881 ILeMeGluLySylMetLySylThrLySylAsnIleAlaLySylIleValaAsnArghPro 900
 Db 2809 ATATATGAAAAAGAAATGAAACCAAGAAATATTTCCAAAGCACTTCAAGAAATAAACCA 2868
 Qy 901 SerLeuIleThrPheLeuCysLySylAsnCysSerValleuAlaCysSerGlyGluAspIle 920
 Db 2869 TCTCTAATTAATCTTTTCCAAAAAATGCAAGTGTGCTAAGCTGTTCTTGGGGAAGATATC 2928
 Qy 921 HisValIleGluLySylMetHisHisValaAsnMetThrProGluPheLySylLeuTyrrIle 940
 Db 2929 CATGTAATGAGAAATGACATCAAGTCAATATGACCCAGAAATTCAGAAACTTACATTT 2988

Qy 941 ValArgGluAsnLySylAlaLeuGlnLySylCysAlaAspTyrrGlnIleAenglyGluIle 960
 Db 2989 GTTAAAGAAACAAAGCACTGCAAAAAGAGTGTCCGACTATCAATTAATGCTGAAATC 3048
 Qy 961 ILeCysLySylCysGlyGlnAlaTrpGlyThrMetCysValaHisLySylLeuAsnLeuPro 980
 Db 3049 ATCTGAAATGTCGCGAGCTTGGGAAACAAATGATGCTCACAAAGGCTTGAATTTGCCCT 3108
 Qy 981 CysLeuLySylAAspAsnPheValaValaPheLySylAsnAsnSerThrLySylGlnTyrr 1000
 Db 3109 TGTCTCAAAATTAAGAAATTTTGTAGTGTGTTTCAAAAATTAATTCACAAAGAAACATAC 3168
 Qy 1001 LySylTyrrValaGluLeuProIleThrPheProAsnLeuAspTyrrSerGluCysCysLeu 1020
 Db 3169 AAAAAGTGGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3228
 Qy 1021 PheSerAspGluAsp 1025
 Db 3229 TTTAGTGAATGAGAT 3243

RESULT 14
 ADJ75813
 ID ADJ75813 standard; DNA; 3771 BP.
 AC ADJ75813;
 XX 20-MAY-2004 (first entry)
 DT 20-MAY-2004 (first entry)
 XX Marker gene SEQ ID NO:11065.
 XX bronchial asthma; chronic obstructive pulmonary disease;
 KM respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KM gene therapy; marker gene; gene; db.
 OS Mus musculus.
 XX EP1394274-A2.
 PN 03-MAR-2004.
 PD 04-ANG-2003; 2003EP-00254857.
 PF 06-AUG-2002; 2002JP-00229312.
 XX 20-MAR-2003; 2003JP-00077212.
 PR (GENO-) GENOX RES INC.
 PA Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 PI WPI; 2004-193155/19.
 XX
 DR Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Claim 14; SEQ ID NO 1065; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 3771 BP, 1183 A; 821 C; 866 G; 901 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3771
Score:	4194.00	Matches:	817
Percent Similarity:	86.9%	Conservative:	75
Best Local Similarity:	79.6%	Mismatches:	132
Query Match:	12	Indels:	2
DB:		Gaps:	2

US-09-515-363c-2 (1-1025) x ADU75813 (1-3771)

QY 1 MetSerAsnGlyTyrSerThrAapGluAsnPhenArgTyrLeuIleSerCysPheArgAla 20
 DB 235 ATGTGATTTGTCTGCTCTGAGAGAGACAGCTTCAGGATCTCATCTTATTTCAAGGCC 234
 QY 21 ArgValIlyMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
 DB 295 AGGCTGAAATGTACATTCAGGTGAGCCAGCTGTCGACCACTCATCTTCTGCTGCA 354
 QY 41 GluValIyGluGlnIleGlnArgThrValAlaThSerGlyAsnMetGlnAlaValGlu 60
 DB 355 GAAACCAAGAGAGATTTCTTAAGAAAGATCAACACCTGTGGTAAACACAGCGGCGGAGAA 414
 QY 61 LeuLeuIleuSerThrIleuGlnIlySGlyValATrPHisleuGlyTrpThrArgGluPheVal 80
 DB 415 CTGCTGCTAGACACTTGGAGAGAGACATGGCCCTGCGGATGGACGCGATGTCGTG 474
 QY 81 GluAlaIleuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
 DB 475 GAGGCCCTAGAGACAGATGCCATCCCTAGCCGCGCTATGTCAAACTCCACACTCATCT 534
 QY 101 AapLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnIleuLeuAsnLeu 120
 DB 535 GATCTGCCCTCTCTCTCTGAGACTGCCATGACAGTGTCTCCACTGCTGACCCCTC 594
 QY 121 LeuGlnProThrLeuValAspIlyLeuLeuValArgAspValIleuAspIlyCysMetGlu 140
 DB 595 CTCACGCCCACTTTGGTGGACAAACTCTGATTAAGATGTCTTGGACACTTGCCTTCGAG 654
 QY 141 GluGluIleuLeuThrIleGluAspArgAsnArgIleAlaAlaIleGluAsnAsnGlyAsn 160
 DB 655 AAGGGACTATTGACAGTCGAGAGAGACAGAAATCGGATTTCTGCTCAGAGAAACACGCGGAAT 714
 QY 161 GluSerGlyValArgGluLeuLeuIlyAspGlyIleValGlnIlyGluAsnTrpPheSerAla 180
 DB 715 GAGTCAGGTGTAAAGAGCTGCTGAGAGAGATTTGTGAGAGAGAAATCGGTTTCTACC 774
 QY 181 PheLeuAsnValIleuArgGlnThrGlyAsnAsnGluLeuValGlnIleuLeuThrGlySer 200
 DB 775 TTCCTGGATTTCTGCGCCCAACTGAAATGATGACTATTCCAGAACTCAACAGGTGGA 834
 QY 201 AspCysSerGlySerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220
 DB 835 GGTGCGCCAGAGAACACAGACACTTGCTCACTCGCTCAAGAGATGGCGCTGACGCT 894
 QY 221 GluGlnIleuLeuLeuSerThrThrValGlnProAsnIleuGluIlySGlyValATrPHisMet 240

DB 895 AATGAGTGTCTTCTGCTGCTGTCATGATGATCAAGTCTGAGACAGAGCGCTGAAACGTA 954
 QY 241 GluAsnAsnSerSerGlySerPheAlaAspSerValIleSerGlySerAspThr 260
 DB 955 GAGCATATTACAGAGAGCTTCTGTACAGATTCCTGTGTACCAAGAAATTCAGACAC 1014
 QY 261 SerLeuAlaGluGlySerValSerCysLeuAspGluSerLeuGlyHisAsnSerAsnMet 280
 DB 1015 AGTTTGGAGAAAGAGATGTACGCTCTTCGATGAAAGCTTGGACATTAACGAAACATG 1074
 QY 281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnVal--AlaAlaArg 299
 DB 1075 GGCAGGAGATTACAGGCACCATGGAAGTATTCAGAGAAAGTGTCTACAGCAAAAGAA 1134
 QY 300 AlaSerProGluProGluIleuGlnIleuArgProTyrGlnMetGlnValAlaGlnProAla 319
 DB 1135 GTATCCCGGAGCAGAACCTGACGCTCAAGCCTTACCAATGAGAGTGGCCCAACAGCT 1194
 QY 320 LeuGluGlyIlyAsnIleIleIleCysLeuProThrGlySerGlyThrArgValAla 339
 DB 1195 CTGATGGAGAAATTTATTTATCTGCTCCCAAGGAGAGTGGAAACAGAGTGGCT 1254
 QY 340 ValTyrIleAlaIlyAspHisLeuAspIlyIlySGlyValAspIleSerGluProGlyIlyVal 359
 DB 1255 GTTACATCACCAAGATCATCTTACAGCAAGAGAGACAGCATCTGAATCCGGGAAGTGT 1314
 QY 360 IleValIleuValAsnIlyValLeuLeuValGluGlnIleuPheArgGluPheGlnPro 379
 DB 1315 ATCGTTCTGTCAATGAAGTAAATGTTAGCAGAACCACTTTCCGAAAGAGTTCAACCCA 1374
 QY 380 PheLeuIlyValTyrPyrArgValIleGlyLeuSerGlyAspThrGlnIleuIlyIleSer 399
 DB 1375 TATTTAAGAAATGGTATGAAATTTAGATTTAAGTGGCGATACCACTGAAATATCA 1434
 QY 400 PheProGluValIlySerCysAspIleIleIleSerThrAlaGlnIleuGluAsn 419
 DB 1435 TTTCCAGAAAGTTGTCAATCTTAACATGTTATATTCAGCAGCTGCTCAAACTCTTGA 1494
 QY 420 SerLeuLeuAsnLeuGluIlySGlyIlyValAspAlaGlyValGlnIleuSerAspPheSerLeu 439
 DB 1495 TCCCTCTTAATCTGAGAGATGAGAGCAGATGACGGGTGTCAGCTGTCAGCTCTCTCTC 1554
 QY 440 IleIleIleAspGluIlySerHisIleThrAsnIlyGluAlaValTyrAsnAsnIleMetArg 459
 DB 1555 ATTATATTGATGATGAGCCATCAACACCAAGAGAGAGTCTTATTAACATCAATGAGA 1614
 QY 460 HisTyrLeuMetGlnIlySerIlyAsnAsnArgLeuIlySGlyIlyAsnIlyProValIle 479
 DB 1615 CGATATTTGAGCAGAGAGCTGAGAAACATTAACCTCAAGAAACAAACCAAGCCATT 1674
 QY 480 ProLeuProGlnIleuGlyLeuThrAlaSerProGlyValGlyIlyAlaThrIlyGln 499
 DB 1675 CCCCTGCCAGATACCTAGAGCTGACAGCTTCACTCGGTGTGGACAGCAGCAAAAGAG 1734
 QY 500 AlaIlyAlaGluGluIlyHisIleLeuIlySGlyAsnValAsnLeuAspAlaPheThrIleIly 519
 DB 1735 TCTGAGCGGAAAGAAATTTTAAATATATGTGCCAACTTGAATGCTTTTACCATTTAA 1794
 QY 520 ThrValIyGluIlyAsnLeuAspGlnIleuIlySGlyAsnGlnIleGlnIlyProCysIlySGlyPhe 539
 DB 1795 ACAGTAAAGAGAAATTTGGTCACTCAAAACCAATTAAGAGAACATGCAAGAAATTT 1854
 QY 540 AlaIleAlaAspAlaThrArgIlyAspProPheIlySGlyIlyLeuLeuGluIlyIleMetThr 559
 DB 1855 GTGATTTGCTGATGACACCAAGAGAAATTCATTTAAAGAGAACATGCAAGAAATTT 1914
 QY 560 ArgIleGlnThrTyrCysGlnIleMetSerProMetSerAspPheGlyThrGlnProTyrGlu 579
 DB 1915 AGCATTCAGACTTACGCAAAAGATCCAAATGTCAGATTTTGAAACCAACTTATGAG 1974
 QY 580 GlnTTPAlaIleGlnIleuGluIlySGlyAlaIlySGlyIlyAsnArgIlySGlyIlyArgVal 599

Dh 1975 CAGTGGCGCATTCAAATGGAGAAAAAGCTGCTAAAGACGGAAATCGCAAGATCGCGTC 2034
Qy 600 CysAlaGluHieLeuArgLysTyrAengLualLeuGlnIleAsnAspThrIleArgMet 619
Dh 2035 TTGTGCAAAACATTTGGAGAGTACCAAGCCCTTCAAAATCAACACAGATCCGAATG 2094
Qy 620 IleAspAlaTyrThrHisLeuGlnThrPheTyrAsnGluGluLysAspLysPheAla 639
Dh 2095 ATTGATGATATATGACCACTGGAGGCAATCTCACTAGATGAGAAAAAGAAAGTTCCGA 2154
Qy 640 ValIleGluAspAspSerAspGluGlyAspAspGluTyrCysAspGlyAspGluAsp 659
Dh 2155 GTCCTC--AATGACAGCGCAAGAGTACAGAGCCACGACTTGCAATGACCACTT 2211
Qy 660 GluAspAspLeuLysPheProLeuLysLeuAspGluThrAspArgPheLeuMetThrLeu 679
Dh 2212 AAGGGCGGATGAAGAAATCTTTGAAATCGAAGAACGATGAATTTCTCATGAATTTGG 2271
Qy 680 PhePheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnProGluTyrGluAsnGlu 699
Dh 2272 TTCTTGATTAACAAGAAAAATGTTGAAAAAATAGTGAATAAACCAAAATACGAGAAATGA 2331
Qy 700 LysLeuThrLysLeuArgAsnThrIleMetGluGlnTyrThrArgThrGluGluSerAla 719
Dh 2332 AACTCATTAATAATTAAGAAACAGATACAGAACTGAACAAATTCACAAAGTCTGAGAGTCTCC 2391
Qy 720 ArgGlyIleIlePheThrLysThrArgGlnSerAlaTyrAlaLeuSerGlnTyrIleThr 739
Dh 2392 CGAGGAATTAATTTTTCACAAAACACAGACAGACCTACGCACTTTCCAGTGGATCATG 2451
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Qy 760 SerSerGluPhePheProMetThrGlnAsnGluGlnLysGluValIleSerLysPheArg 779
Dh 2512 AGCAGTGAAGTCAAGGCCAGTACTGACTGAGTCAACAAAGAAATCAATTAATTTTCGC 2571
Qy 780 ThrGlyLysIleAsnLeuLeuIleAlaThrThrValAlaGluGluLysLeuAspIleLys 799
Dh 2572 ACTGGGAAATTAATTCGCTTAATCGCTACGACGCTGGCAGAGAAAGCCGCGATATCAAA 2631
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Dh 2632 GAGTGCAATATTTGTATTCGTTATGCGCTTGTCACCAACGAGATAGCAGTGTCCAGGCC 2691
Qy 820 ArgGlyArgAlaArgAlaAspGluSerThrTyrValLeuValAlaHisSerGlySerGly 839
Dh 2692 CCGGGTCGAGCCGAGCTGATGAAGCAGATATGCTCTGCTCCAGCCAGCGAGTGGCTCAGGA 2751
Qy 840 ValIleGluHieGluThrValaAsnAspPheArgGluLysMetMetTyrLysAlaIleHis 859
Dh 2752 GTTACCGAAGCGGAGATGTTGTAATGATTTCCGAGAGAAGATGATTAAGGATTAATTA 2811
Qy 860 CysValGluAsnMetLysProGluGluTyrAlaHisLysIleLeuGluLeuGlnMetGln 879
Dh 2812 CGTGTTCAAAAACATGAACAACAGAGAGTATGCAATTAAGATTTTGGATTTGCGAGTGC 2871
Qy 880 SerIleMetGluLysLysMetLysThrLysArgAsnIleAlaLysHisTyrLysAsnAsn 899
Dh 2872 AGTATCTGGAAGAAAGAAATGAAGATGCAAAAGAAATTCGAAAGCAATTAACAGCAACAT 2931
Qy 900 ProSerLeuIleThrPheLeuLysCysLysAsnCysSerValLeuAlaCysSerGlyGluAsp 919
Dh 2932 CCAATCTTAATAACACTTCTCTCCAAAATTTGTAGCATGTGTGTCTCTCGGAGAAAC 2991
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Dh 2992 ATCCATGTCAATTAGAGAGATGATCATGTCAATATATGACACAGAAATTCAGAGGACTTAC 3051
Qy 940 IleValArgLysAlaLeuGlnLysLysCysAlaAspTyrGlnIleAsnGlyGlu 959
Dh 3052 ATTGTAAAGAAAAACAAGCACTGCAAAAGAAATTTGCTGATTATCAGACCAATGGAGAG 3111

Qy 960 IleIleCysLysCysGlyGlnAlaTyrGlyThrMetMetValHisLysGlyLeuAspLeu 979
Dh 3112 ATTATCTGCAAGTGTGCGCAGGCTTGGGAAACAAATGATGTGCACAAAGTTAGATTGG 3171
Qy 980 ProCysLeuLysIleLeuArgAsnPheValValValPheLysAsnAspSerThrLysLysGln 999
Dh 3172 CTTTGCTTAATAATAAGAAATTTGTATGATCAATTTCAAAAATTAATCACTACCGAAGAAACAG 3231
Qy 1000 TyrLysLysTyrValGluLeuPheProIleThrPheProAsnLeuAspTyrSerGluCysCys 1019
Dh 3232 TACAAAGATGGGTGGAATTTGCTTATCAGATTTTCCGATCTTGACTACTCAGAAATACTCG 3291
Qy 1020 LeuPheSerAspGluAsp 1025
Dh 3292 TTGTATATGATGAATGAAT 3309
RESULT 15
AAS40960
ID AAS40960 standard; cDNA, 1967 BP.
AC AAS40960;
XX
DT 17-DEC-2001 (first entry)
XX
DE cDNA encoding novel human enzyme polypeptide #176.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ss.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001, 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 11-JUL-2000; 2000US-0217496P.
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PR 26-JUL-2000; 2000US-0220963P.
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PR 23-AUG-2000; 2000US-0227009P.
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PR 08-SEP-2000; 2000US-0231242P.
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PR 14-SEP-2000; 2000US-0232397P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 20-OCT-2000; 2000US-0241809P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 06-DEC-2000; 2000US-0256719P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465566/50.
XX P-PSDB; AAU23090.
DR
XX
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neutral, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Claim 4; SEQ ID NO 166; 1180bp; English.

XX The present invention relates to the isolation of novel human enzyme
XX polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
XX encoding them. The enzyme polypeptides of the invention may comprise the
XX functional classes of oxidoreductases, transferases, hydrolases, lyases,
XX isomerases or ligases. The sequences of the invention are useful in the
XX diagnosis, treatment, prevention and/or prognosis of a wide range of
XX disorders including hyperproliferative disorders (e.g. cancer),
XX immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
XX arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
XX disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
XX cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
XX (e.g. haemophilia), reproductive disorders (e.g. infertility) and
XX infectious disorders (e.g. influenza). The polynucleotides of the
XX invention can also be used in gene therapy. AA540765-AA541684 represent
XX cDNA sequences encoding for the novel human enzyme polypeptides of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 1967 BP; 723 A; 344 C; 416 G; 476 T; 0 U; 8 Other;
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Score: 3176.00 Matches: 636
Percent Similarity: 97.1% Conservative: 2
Best Local Similarity: 96.8% Mismatches: 18
Query Match: 59.8% Indels: 5

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US-09-515-363C-2 (1-1025) x AAS40960 (1-1967)

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      63  GAAAGTGGCCAGCCAGCTTGGAAAGGAAATATCATCTGCTCCCTTACAGGAGT 122
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QY      334  GlyLeuThrArgValAlaValTyrIleAlaYAspHisLeuAspLysLysVala 353
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      123  GGAATAACCAAGAGTGGCTGTTTACATTGCCAAGATCACTTAGACAAGAAAAAGCA 182
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QY      354  SerGluProGlyLysValIleValLeuValAsnLysValLeuValGluGlnLeuPhe 373
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QY      374  ArgLysGluPheGlnProPheLeuLysLysTyrTyrArgValIleGlyLeuSerGlyAsp 393
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      243  CGAGAGAGTTCACACCATTTTGGAGAAATGGTATCGTCTTATGGATTAACTGGTAT 302
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QY      394  ThrGlnLeuLysIleSerPheProGluValValLysSerCysAspIleIleIleSerThr 413
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      303  ACCCACTGAAATATCATTTCCAGAAAGTTGCAAGCTCGTATATTATTATCATGACA 362
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QY      414  AlaGlnIleLeuGlnLysSerLeuLeuAsnLeuGlnAsnGlyLysAspAlaGlyValGln 433
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      363  GCTCAATCTTTAAAACTCCCTTAACTGTAAGTGAAGAGTGGTGGTTCAA 422
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      1263  AGGACTGAGGAATCAGACAGAGAAATATCTTTACAAAAACAGACAGTGCATATGGG 1322
      |||
QY      734  LeuSerGlnTyrIleThrGluAsnGluLysPheAlaGluValGlyValLysAlaHisHis 753
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Search completed: March 12, 2006, 22:52:31

Job time : 2545 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: March 13, 2006, 15:21:08 ; Search time 9400 Seconds
(without alignments)
5101.783 Million cell updates/sec

Title: US-09-515-363C-2

Perfect score: 5311
Sequence: 1 MNGXYSTDENFRYLSCFRA.....LPITFENLDYSECLFSDSD 1025

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB.spool/US09515363/runat_10032006_181130_7973/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODB=LOCAL
-OUTFMT=pcp -NORM=ext -HEADING=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss604
-USER=US09515363 @CGN_1_1_5315@runat_10032006_181130_7973 -NCPD=6 -ICPD=3
-NO_MMAL -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
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7: gb_est6:*
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9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5250	98.9	3078	11	DQ050960 Homo sapi
2	4879	91.9	3078	11	DQ050961 Pan trogl
3	2673	50.3	2304	4	AK037057 Mus muscu
4	2633	49.6	2331	4	AK040519 Mus muscu
5	1597	30.1	1013	4	BQ233683 AGENCOURT
6	1376	25.9	870	5	BQ960157 AGENCOURT
7	1366	25.7	2530	4	CR857114 Pongo pyg

8	1289.5	24.3	918	5	BU189982
9	1257	23.7	1174	5	BU902097
10	1218	22.9	1115	3	BM467983 AGENCOURT
11	1206.5	22.7	1035	2	BF337464
12	1186	22.3	690	8	DR422160
13	1129	21.3	729	2	BF983236
14	1122	21.1	972	5	BY720783
15	1122	21.1	1197	4	AK018602
16	1098	20.7	827	2	BG741146
17	1094.5	20.6	781	2	BF686405
18	1083	20.4	653	7	CR752055
19	1081.5	20.3	1041	2	BE882040
20	1078	20.4	627	5	BX492926
21	1066	20.1	1046	3	BM476961
22	1059	19.9	755	5	BO772836
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24	1045	19.7	4098	4	BC070029
25	1021.5	19.2	800	7	CO396840
26	1019	19.2	582	1	AU310289
27	1016	19.1	672	3	BQ316075
28	1016	19.1	672	3	BQ316108
29	1016	19.1	672	3	BQ316120
30	994	18.7	671	6	CB453859
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32	990	18.6	672	6	CA339255
33	989.5	18.6	672	6	BM455238
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35	954	18.0	682	6	CF363618
36	952.5	17.9	932	2	BG967530
37	949.5	17.9	585	3	BP210040
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ALIGNMENTS

RESULT 1	DQ050960	3078 bp	DNA	linear	GSS 02-JUN-2005
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DEFINITION	Homo sapiens MDAS gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	DQ050960				
VERSION	DQ050960.1	GI:66904159			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3078)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Friedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.				
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees				
JOURNAL	(er) PLOS Biol. 3 (6), E170 (2005)				
PUBMED	15869325				
REFERENCE	2 (bases 1 to 3078)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Friedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Substitution				
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gate Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				

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/locus_tag="HC18981"

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Percent Similarity: 99.1% Conservative: 1
Best Local Similarity: 99.0% Mismatches: 9
Query Match: 98.9% Indels: 0
DB: 11 Gaps: 0

US-09-515-363C-2 (1-1025) x DQ050960 (1-3078)

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QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
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QY 41 GluValIleGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
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DB 181 CTGCTGCTAGCACTTGGAGAGGAGTCTGCACTTGTTGGACTGGGAATTCGTG 240
QY 81 GluAlaIleuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
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DB 301 GACTGCCCTCTCCATCGTTTGAGAACGCTCATGATGAATATCTCAACTGCTGAACCTC 360
QY 121 LeuGlnProThrLeuValAspIleLeuLeuValArgAspValLeuAspIleCysMetGlu 140
DB 361 CTTCAGCCCACTCTGGTGGCAAGCTTCTAGTTAGACGCTTGGATTAGTGCATGAG 420
QY 141 GluGluLeuLeuThrIleGluAspArgAsnArgIleAlaAlaIleGluAsnAsnGlyAsn 160
DB 421 GAGGAACCTGTGACATTTGAAGACAAACCGGATTCGCTGCTCAAAAACATGAAAT 480
QY 161 GluSerGlyValArgGluLeuLeuIleValIleValGlnIleGluLeuAsnTrpPheSerAla 180
DB 481 GAATCAGGTGTAAAGAGCTACTAAAGAGATGTGCAGAAAGAAAATCGTCTCTGCA 540
QY 181 PheLeuAsnValLeuArgGlnThrArgIleAsnAsnGluLeuValGlnIleuThrArgIleSer 200
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DB 601 GATGTGCTCAGAAAGCAATGAGAGATTGAGAAATTTATCACAACTGATGCTCTCAAGT 660
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QY 461 TyrLeuMetGlnIleLeuIleValAsnAsnArgIleValIleValGluAsnIleProValIlePro 480
DB 1381 TATTGATGCAAGAAAGTTGAAGAAACATTAAGCTCAAGAAAGAAACAAACAGTATCCC 1440
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DB 1441 CTTCCCTCAGATCTGGACTTAACAGCTTCACTGGGTGTTGAGGGGCCACGAAGCAAGCC 1500
QY 501 IysAlaGluGlnHisIleLeuIleIleCysValAsnLeuAspAlaPheThrIleIleThr 520
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DB 1621 ATTCAGATGCAACAGAGAAATCATCTTAAGAGAAACCTTGAATAATATGACAAAG 1680
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DB 1681 ATTCAAACTTATTTGCAATATGAGTCAATGTGAGATTTTGGAACTCAACCCATATGAAACA 1740
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DB 1741 TGGGCATTCAATGGAAGAAAAAGCTGCAAAAGAAAGAAATCGCAAGAAAGCTGTTGT 1800
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QY 621 AspAlaTyrThrHisIleuGlnIleThrPheTyrAsnGluGluIleValAspIleValIleVal 640

Qy 61 LeuLeuLeuSerThrIeuGluIuYsGluYVal1TrpHisLeuGluYTrpThraArgGluPheVal 80
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Qy 81 GluAlaLeuAraArgThrGlySerProIeuAlaAlaArgTyMetSerProGluLeuThr 100
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Db 301 GACTTGCCCTCTCCATCGCTTTGAGAACGCTCATGATATCTCCAACTCGTGAACCTC 360
Qy 121 LeuGluProThrLeuValAspLyLeuLeuValArgAaspValLeuAspLyCysMetGlu 140
Db 361 CTTCAGCCCACTCTGGTGGAAGCTTCTAGTTAGAGACGCTTGATAGTCAATGAGAG 420
Qy 141 GluGluLeuLeuThr11eGluAaspAraAraGlu11aAlaAlaGluLeuAenGluYan 160
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Db 481 GAGTCAGGTGTAGAGAGCTACTAAAGAAGATTGTGACAGAAAGAACTGTTCTCTGCA 540
Qy 181 PheLeuAenValLeuArgGluInThrGlyAenAenGluLeuValGluGluLeuThrGlySer 200
Db 541 TTTCTGAATGTTCTTCTGTCMAACAGGAAACAATGAATCTTCCAAAGATTAAACAGGCTCT 600
Qy 201 AapCysSerGluSerSerAlaGlu11eGluAenLeuSerGluValAaspGluProGluVal 220
Db 601 GATTGCTCAGAAAGCAATGCAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 660
Qy 221 GluGluGluIleuLeuSerThrThrValGluProAenLeuGluYsGluVal1TrpGluYmet 240
Db 661 NNN 720
Qy 241 GluAenAenSerSerGluSerSerPheAlaAaspSerValYalSerGluSerAapThr 260
Db 721 NNA 780
Qy 261 SerLeuAlaGluGluYserValSerCysLeuAaspGluSerLeuGluYHisAenSerAenMet 280
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Db 901 TCCCCGGAAGCCAGAACTCCAGCTCAGGCCCTTACCAATGGAAAGTTGCCCGACGCCCTTG 960
Qy 321 GluGluYlyAenAla11e11eCysLeuProThrGlySerGluYlySerThraArgValAlaVal 340
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Qy 341 Tyr11aAlaYsAaspHisLeuAaspLySlySlyLeuYalAserGluProGluYlyVal11e 360
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Qy 361 ValLeuValAenLySlyValLeuLeuValGluGluLeuPheArgLySgluPheGluProPhe 380
Db 1081 GTTCTTGTCAATAGGTAAGTCTAGTTGAACAGCTCTTCGCAAGAGGTCCAAACCATTT 1140
Qy 381 LeuLySlyeTrpTyTrArgVal11eGluYLeuSerGluYAspThrGluIleuYs11eSerPhe 400
Db 1141 TTGAAAGAAATGATGATGTATTAGATTAGAGGTATACCCAACTGAAAAATATCATTT 1200
Qy 401 ProGluValYalYsSerCysAasp11e11eSerThra1aGluIn11eLeuGluAenSer 420
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Db 1321 ATCATTTGAATGATGATCATCAACCAAGAAAGAGGTATATATATCACTATGAGGCGT 1380
Qy 461 TyrLeuMetGluYlyLeuAenAenAraGLeuYlySgluAenLySProVal11ePro 480
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Qy 481 LeuProGluIn11eLeuGluYleuThrYalSerProGluYValGluYalThrYsGluAla 500
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Qy 501 YsAlaGluGluYHis11eLeuYlySerCysAlaAenLeuAaspAlaPheThr11eYlyThr 520
Db 1501 AAAGCTGAAGAACACATTTTAAACATATGTGCCAATCTTGATGCAATTTCTATTAACCT 1560
Qy 521 ValYlyGluAenLeuAaspGluLeuYsAenGlu11eGluProCysYlySlyPheAla 540
Db 1561 GTTAAAGAAACCTTGATCACTGAACCAAAATPACAGAGCCATGCAAGAAATTTGCC 1620
Qy 541 11eAlaAaspAla11eThraGluAaspProPheYsGluYlyLeuGluY11eMetThraArg 560
Db 1621 ATTGCAGATGCAACAGAGAAAGATCCATTTAAAGAGAAACCTNNAGAAATTAATGACAAAG 1680
Qy 561 11eGluInThrTyCysGluYmetSerProMetSerAaspPheGluYThrGluProTyGluGlu 580
Db 1681 ATTCAAACTTATTTGTCAATATGAGTCCAAATGTCAAGATTTTGGAACTCAACCTATGAACA 1740
Qy 581 TrpAla11eGluYmetGluYlySlyValAlaYlySlyGluYsAraGlySgluYVal1Cys 600
Db 1741 TGGGCATTTCAATGGAAAAAAGAGCTGCAAAAGAAAGAAATCGCAAAAGAGCTGTTGT 1800
Qy 601 AlaGluHisLeuAraGluYerThraAenGluYalAenAaspThr11eArgMet11e 620
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Qy 641 11eGluAaspAaspSerAaspGluGluYlyAaspGluYTyCysAaspGluYalAaspGlu 660
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Qy 661 AaspAaspLeuYlyYerProLeuYlySlyAaspGluInThrAaspArgPheLeuMetThrLeuPhe 680
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Qy 681 PheGluAenAenLyMetLeuYsAraGLeuAlaGluAenProGluYTyGluAenGluYly 700
Db 2041 TTTGAAAAACAATGAATGTTGAAAAAGCTGGCTGAAAAACCGAATATGAATAATGAAAAAG 2100
Qy 701 LeuThrYlyLeuAraGluInThr11eMetGluGluYTyTrpThraArgThruGluSerAlaArg 720
Db 2101 CTGACCAATTTAAGAAATATACCAATATGAGCAATATATCAAGATGAGGAAATCAGACACA 2160
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Oy	801	CybaenlllevalleatrgTgelyeuValthrasmguillealmetValglmlaarg	820
Db	2401	TGTAAACATGTTATCCGTTATGCTCGTCGCACCAATGAAATAGCCATGTMNNGCCCGT	24600
Oy	821	GlYArGAlaArGAlaAspGluSerThrTrYrValleuValalAhleSerGluSerGlyAla	840
Db	2461	GSTCAGCGCAGAGCTGATGAGAGCACCTTACGCTCGTGTTGCTCACAGCGGTTCCAGAACTT	25200
Oy	841	llegluHleSgluThrValAsnaSppheArgrgluylsmetMetYrGlyAlalAlelSgys	860
Db	2521	ATCGAACGTGAGACAGCTTATATCATTTCCGAGAGAAAGATGATATTAAGACTTATACATTGT	25800
Oy	861	ValGlnaenmetLysProgluGluTrYrAlAhlsylsilleuGluLeuGlnmetGlnSer	880
Db	2581	GTTCAAAATATGCAACCAAGAGATGATGCTCATAGATTTTGAAATTCACAGTGCAAAGT	26400
Oy	881	llemetGluYrlybysmetLysThrlyAsrArgaenllealalyshleTyrlyAsnaSppro	900
Db	2641	ATAATGGAAGAAAGAAATGAAAAACCAAGAGAAATATTTGCCAAGCATTTACAGAAATPACCA	27000
Oy	901	SerleuileThrPheleuCyelysaSnCysSerValleuAlaCysSerGlyGluAspIle	920
Db	2701	TCACTATATACCTTCTTCCTTGCAAAACCTGCAGTGTGCTAGCTGTCTTGGGGAGATATTC	27600
Oy	921	HlsValillegluYrsmethshlsValaSnmetThrProgluPheylsGluYrIle	940
Db	2761	CACGTAATTTAGAAAATGATCATCAGTCAATATGACCCAGAAATTCAGAACTTTACATT	28200
Oy	941	ValArgrgluAenlybAlaleuGlnlyblyScySalasppYrGlnlleasnglyGluIle	960
Db	2821	GTAAGAGAAAAACAAAGCACTGCACAAAGAAAGTGTGCCACTATCAAAATTAATGTGAAATC	28800
Oy	961	lleCyelysCySglYGlAlaATroglYthrmetMetValHlsylsGlyLeuAspLeuPro	980
Db	2881	ATTCGCAAAATGTGGCCAGGCTTTGGGGAAACAATGATGTGTGCACAAAGGCTTATGATTTGCTT	29400
Oy	981	CysleuYrilleArGAsnPheValValPheylsaSnasSerThrlyblySgluTr	10000
Db	2941	TGTCTCAAAATPAGAAATTTTGTAGTGTGTTTCAAAAATTAATTCACAAAGAAACAATAC	30000
Oy	1001	LyslySTrPValGluLeuProilleThrPheProaenleuAspYrSerGluCySyleu	10200
Db	3001	AAAAAGTGGGTAGAAATTACTTATCATCATTTCCCAATCTTGACTATTCAGAAATGCTGTTTA	30600
Oy	1021	PheSerAspGluAsp 1025	
Db	3061	TTTTTGTAGTGAAGAGAT 3075	
RESULT 3			
LOCUS	AK037057	2304 bp	mRNA linear HTC 03-APR-2004
DEFINITION			Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930105804 product:similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens], full insert sequence.
ACCESSION	AK037057		
VERSION	AK037057.1	GI:26331913	
KEYWORDS			HTC; CAP trapper.
SOURCE			Mus musculus (house mouse)
ORGANISM			Mus musculus
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			
AUTHORS			Carninci,P. and Hayashizaki,Y.
TITLE			High-efficiency full-length cDNA cloning
JOURNAL			Meth. Enzymol. 303, 19-44 (1999)
PUBMED			10349636
REFERENCE			
AUTHORS			Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	11042159
AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasukawa, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Ozaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	11076861
AUTHORS	4 THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	THE FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2304)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiwamoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohnato, N., Ozaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaru-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yaeunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, url: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
COMMENT	Please visit our web site for further details.
COMMENT	URL: http://genome.gsc.riken.jp/
COMMENT	URL: http://fantom.gsc.riken.jp/
COMMENT	Location/Qualifiers
FEATURES	1. 2304
SOURCE	/organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM:DB:9930105B04" /db_xref="taxon:10090" /clone="9930105B04" /sex="female" /tissue_type="vagina" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 224. .->2302 /note="unamanged protein product; putative similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens] (SPTPR Q9H366, evidence: PASTY, 75.6%ID, 67.6%length, match=2079)"
CDS	

Db 1964 CAGTGGCCCATTCMAATGAGAAAAAGCTGCTAAAGACGAAATCGCAAGATCGCGTC 2023

Qy 600 CysAlaGluHisLeuArgHisTyrAngluAlaLeuGlnIleAspAspThrIleArgMet 619

Db 2024 TGTGCAAAACATTTGGAGATCAACGAAGCCCTCAATCAACACACGATCCGAATG 2083

Qy 620 IleAspAlaTyrThrHisLeuGluThrPheTyrAsnGluLysAspHisPheAla 639

Db 2084 ATTGATGCATATAGCCACTGAGACATTTCTACACGATGAGAAAGAAAGATTCCGA 2143

Qy 640 ValIleGluAspSerAspGluGlyGlyAspAspGluTyrCysAspGlyAspGluAsp 659

Db 2144 GTTCCTC---AATGACGACCAACAAAGCTGATGACGAGCCACGATTCGCAATGCAACTT 2200

Qy 660 GluAspAspLeuLysPheProLeuLysLeuAspGluThrAspArgPheLeuMetThrIleu 679

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Qy 680 PhePheGluAspAsnLysMetLeuLysArgLeuAlaGluAsn 693

Db 2261 TTCTTTGATACAGAAATGTTGAAAAAAGCTGCTGAAAC 2302

RESULT 4 AK040519 2331 bp mRNA linear HTC 03-APR-2004

LOCUS AK040519 Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone: A430105A06 product: similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 (Homo sapiens), full insert sequence.

ACCESSION AK040519 GI:26333792

VERSION AK040519.1 GI:26333792

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

JOURNAL PUBMED 10349636

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL PUBMED 11042159

REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sum, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, H., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, E., Ohara, E., Wachihi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL PUBMED 11076861

REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

JOURNAL REFERENCE 5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

JOURNAL REFERENCE 6 (bases 1 to 2331)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozumi, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanakawa, T., Kato, H., Kawai, D., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyachi, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUN-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sec.riken.jp, URL: http://genome.sec.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.sec.riken.jp/

URL: http://fantom.sec.riken.jp/

URL: http://fantom.gen.riken.jp/

FEATURES

source

1..2331

location/Qualifiers

organism="Mus musculus"

mol_type="mRNA"

strain="C57BL/6J"

db_xref="PANTOM_DB:A430105A06"

db_xref="taxon:10090"

clone="A430105A06"

tissue_type="thymus"

clone_lib="RIKEN full-length enriched mouse cDNA library"

dev_stage="0 day neonate"

dev_2331

/note="unnamed protein product; putative similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 (Homo sapiens) (SPTK109H3G6, evidence: FASTV, 75.6%ID, 67.6%length, match=2079)"

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CDS

ORIGIN

Alignment Scores:

Pred. No.: 7.06e-271

Score: 2633.00

Percent Similarity: 84.2%

Best Local Similarity: 75.6%

Query Match: 49.6%

DB: 4

US-09-515-363c-2 (1-1025) x AK040519 (1-2331)

Qy 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla 20

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Db      283  ATGTCATTTGTCGTCTGTCAGAGGACACCTTCAGGAATCTCATCTTATTTCTTCAGGCC 342
Qy      21  ArgValIyMeTyrTrIleGlnValGlnProValIleuAspTyrIleuThrPheIleuProAla 40
Db      343  AGCGTAAATATGACACTTCAGTGGAGCCAGTGTCTGACCACTTCCTTCTGTCGCA 402
Qy      41  GluValIyGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
Db      403  GAAACCAAGAGAGAGTTCTTAAGAAAGATCAACCTGTGGTAAACACAGCGCGGACAA 462
Qy      61  LeuLeuLeuSerThrIleuGlnIyGlyValTyrPheIleuGlyTyrThrArgGlnPheVal 80
Db      463  CTGCTGCTAGCACCCTTGGAGCGAGCAATGCGCTTGGATGAGCGACAGATGTCGCG 522
Qy      81  GluAlaIleuArgArgThrGlySerProIleuAlaAlaArgTyrMetAsnProGluIleuThr 100
Db      523  GAGGCCCTTAGACACAGTGGCAATCCCTAGCCGCGCTATGTCAAAACCCACACTCACT 582
Qy      101  AspLeuProSerProSerPheGluAsnAlaIleAspGluTyrIleuGlnIleuLeuAsnLeu 120
Db      583  GATCTGCCCTCTCTCTCTCTGAGACTGCCCATGAGAGTGTCTCACCTTGTGACCCCTC 642
Qy      121  LeuGlnProThrIleuValIlePylIyLeuLeuValArgAspValIleuAspIyIyCysMetGlu 140
Db      643  CTCAGCCCACTTGGTGGACAAACTTCGATTAACAGTGTCTTGGACACTTGTCTCGAG 702
Qy      141  GluGlnIleuLeuThrIleGlnAspArgAsnArgIleAlaAlaIleGlnAsnAsnGlyAsn 160
Db      703  AAGGACCTATTTGACAGCTGACAGACAGAAATCGGATTTCTGTCAGAGAAACACCGGAAAT 762
Qy      161  GluSerGlyValArgIleuLeuLeuIyValArgIleValGlnIyGlnAsnIleuAsnIleuPheSerAla 180
Db      763  GAGTCAGGTGTAGAGAGAGCTGCTGAGAGAGATTTGTCAAGAGGAAAACCTGTTTCTAC 822
Qy      181  PheLeuAsnValIleuArgGlnThrGlyAsnAsnGlnIleuValGlnGlnIleuThrGlySer 200
Db      823  TTCCTGATGTCTTCTGCGCCAACTGGAATGATGCACTATTCMAAATACTMAACGGGTGCA 882
Qy      201  AspCysSerGluSerAsnIleGlnIleGlnAsnIleuSerGlnValIleAspGlyProGlnVal 220
Db      883  GCGTCCCAAGAACACACAGACTTGTACTCTGCTCACAGAGAGTGGGCTCGCACT 942
Qy      221  GluGlnGlnIleuLeuSerThrThrValGlnProAsnIleuGlnIyGlnValIlePylIyMet 240
Db      943  AATGATGTCTTCTGCTGCTGCTGCTGATGATCAAGCTGAGACAGAGCGCTGGAACGTA 1002
Qy      241  GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValIleSerGluSerAspThr 260
Db      1003  GACGACATATTACACAGAGGCTTCTGTACAGATTCTGTGTGACCAACAGATACAGACACA 1062
Qy      261  SerLeuAlaGlnIySerValIleSerCysIleuAspGluSerIleuGlnIleAsnSerAsnMet 280
Db      1063  AGTTTGGCAGAGAGAGTGTCACTGCTGCTGATGAAGTCTTGACATTAACACACACATG 1122
Qy      281  GlySerAspSerGlyThrMetGlySerAspSerAspGlnIleuAsnValIleAlaIleArg 299
Db      1123  GCGAGGAGATTCAAGCACATGGGAGATGATTCAGATGAAGTGTCAATCCAGACAAAAGA 1182
Qy      300  AlaSerProGluProGluIleuGlnIleuArgProTyrGlnMetGlnValAlaIleProAla 319
Db      1183  GATCCCGCCGAGCCAGAACTGACAGCTCAAGGCTTACCAAAATGGAAGTGGCCCAACGACT 1242
Qy      320  LeuGlnGlyIyAsnAsnIleIleIleCysIleuProThrGlySerGlyIyThrArgValAla 339
Db      1243  CTAGATGGGAAAGATATTATATCTGCTCCCAAGGAGGTGGGAAACCAAGATGGCT 1302
Qy      340  ValTyrTrIleAlaIyAspPheIleuAspIyIyIyLeuIyIyLeuIleAspGluProGlyIyVal 359
Db      1303  GTTTACATCACCAAGATCACTTAGACAAAGAGAGGCACTGAATCCGGGAAGCTT 1362
Qy      360  IleValIleuValAsnIyValIleuLeuValGlnGlnIleuPheArgIyGlnPheGlnPro 379

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Db      1363  ATCGTTCTTGTCAATTAAGSTAAATGTTAGCAGAACACTTTTCCGAAGAAAGTTCAACCA 1422
Qy      380  PheLeuIyIyIyIyIyIyIyIyIyIleGlnValIleGlyIleuSerGlyAspThrGlnIleuIyIyIySer 399
Db      1423  TATTTGAAGAAATGGATATGATTAATGATTAATGAGGAGATACCACTGAAATATATCA 1482
Qy      400  PheProGluValValIyIyIyIyIyIyIleIleIleIleIleIleIleIleIleIleIleIleIle 419
Db      1483  TTTCCAGAAAGTTGTCAATCTTAACAGATGTTATATCAAGCACTGCTCAAAATCTTGAAGAC 1542
Qy      420  SerLeuLeuAsnIleuGlnIyGlnIleuAspAlaGlyValIleGlnIleuSerAspPheSerLeu 439
Db      1543  TCCCTCTTAATCTGAGAGGTGAGACAGATGACAGGTGTGACAGCTGCTCAACTTCTCTC 1602
Qy      440  IleIleIleAspGluCysIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 459
Db      1603  ATTTATCATTTGATGAGTGGCATCACACCAAGAGAGGAGTGTATTAACAATCATGAGAGA 1662
Qy      460  HisTyrLeuMetGlnIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 479
Db      1663  CGATATTTGACAGACAGAGCTGAGAAACATGACCTTCMAAGAACAAACCAACGACCATT 1722
Qy      480  ProIleuProGlnIleIleuGlyIleuThrAlaSerProGlyValIleGlyValIleThrIyIyGln 499
Db      1723  CCCCTGCCAGATACTAGAGACTGACAGCTTCACTGCTGTGGAGACGACCAAAAGCAG 1782
Qy      500  AlaIyIyAlaGluGlnIleIleIleuIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 519
Db      1783  TCTGAGGCTGAAAACATATTTTAATATATGTGCCAATCTTGATGCTTTACATTAATA 1842
Qy      520  ThrValIyGlnIleuAsnIleuAspGlnIleuIyIyIyIyIyIyIleGlnIleuProCysIyIyIyPhe 539
Db      1843  ACAGTGAAGAGAAATCTTGTCAACTCAACCAACCAAAATGAAGAACCAATGACAAAGAAATTT 1902
Qy      540  AlaIleAlaAspAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 559
Db      1903  GTGATTTGCTGATGACACCAAGAAATCCATTTAAAGAGAACTTCAAGAAATTAATAGCA 1962
Qy      560  ArgIleGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGln 579
Db      1963  AGCATTCACACTTACTGCCAAAAGTCCAAATGTCAATTTGGAAACCAACATTAATGAG 2022
Qy      580  GlnTTPAlaIleGlnMetGlnIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 599
Db      2023  CAGTGGCCATTCAAATGAGAAAGAGTGTCTAAAGACGGAATGCAAGAAATGCGCGTC 2082
Qy      600  CysAlaGlnHisIleuArgIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 619
Db      2083  TGTGCAGAACATTTGAGAAAGTACAGAGCCCTTAACATCAACAGACAGATCCGAATG 2142
Qy      620  IleAspAlaTyrThrHisIleuGlnIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 639
Db      2143  ATTTGATGACATATAGCACTGGAGACATTTCTACATGATGAGAAAGAAAGATTCGCA 2202
Qy      640  ValIleGlnAspAspSerAspGlnIyGlyIyAspAspGlnIyIyIyIyIyIyIyIyIyIyIyIyIy 659
Db      2203  GTCTCTC---AATGACAGCCACAAAGTGTAGAGAGGACGACGAGTTCGAATGACCAACTT 2259
Qy      660  GluAspAspLeuIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 679
Db      2260  AAGGGGAGTGTAAAGAAATCTTTGAACCTGAGCAAGACGATGAATTTCTCATGAATTTG 2319
Qy      680  PhePheGluAsn 683
Db      2320  TTCTTTGATTAAC 2331

```

RESULT 5
 BQ233683 1013 bp mRNA linear EST 02-MAY-2002
 LOCUS BQ233683
 DEFINITION AGENCOURT_7258428 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5786526
 5' mRNA sequence.
 ACCESSION BQ233683
 VERSION BQ233683.1 GI:20415083

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 1013)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12875 row: 9 column: 07
High quality sequence stop: 721.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5786526"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Alignment Scores:
Pred. No.: 3,88e-160 Length: 1013
Score: 1597.00 Matches: 322
Percent Similarity: 95.6% Conservative: 5
Best Local Similarity: 94.2% Mismatches: 9
Query Match: 30.1% Indels: 8
DB: 3 Gaps: 3

US-09-515-363c-2 (1-1025) x BQ233683 (1-1013)

QY 529 lvsAsnglnllecInguProCyslyslsPheAlaIleAlaapAlaThrArgGluasp 548
DB 2 AAAAACCAATACAGGAGCCATCAAGAGTTGCCATTGCAGATGCACAGAGAAAT 61
QY 549 ProPhelsglulysleuIeuGluIleMetThrArgIleGlnThrTyrcysglImetSer 568
DB 62 CCATTAAAGAGAACTCTAGAAATATATGACAAAGATTCAACTTATTTGCAATGAGT 121
QY 569 ProMetSeraspPheglYThrInProTyrglGlnTrpAlaIleGlnMetGluTylys 588
DB 122 CCATGTGAGATTGGAATCAACCTATGAAACAATGGCCATTCAATGAGAAAAA 181
QY 589 AlaAlaIysglIysenArglysgIuArgValCysAlaGluHisleuArglysTyra 608
DB 182 GCTGCAAAAGAGAAATCGCAAGAAACGTTTGTGCAAGAACATTTGAGAGATCAAT 241
QY 609 GluAlaIeuGlnIleasnAspThrIleArgMetIleAspAlaTyThrHisleuGluThr 628
DB 242 GAGGCCCTACAAATTAATGACACAAATTCGATATGATATCATCTTCTTGAAC 301
QY 629 PheTyraSnglnlguIysAspIysPheAlaValIleGluAspAspSerAspGluGly 648
DB 302 TTTCTATATATGAAGAGAAAGTAAAGACTTTGCGATCTATGAAGATGATGATGAGG 361
QY 649 GlIyAspAspGluTyrcysAspGlyAspGluAspGluAspAspLeuTylysProleuTy 668
DB 362 GGTGATGATGAGATATTGTGATGATGATGATGATGATGATGATGATGATGATGAT 421

QY 669 LeuAspGluThrAspArgPheLeuMetThrIleuPheGluAsnAsnIysMetLeuTy 688
DB 422 CTGGATGAAACAGATGATGATTTCTCATGACTTTATTTTGAAGAAACATTAATGTTGAA 481
QY 689 ArgLeuAlaGluAsnProGluTyrgluAsngluTylysLeuThrIlyLeuArgAsnThrIle 708
DB 482 AGCTGTGCGAAACCCAGAAATATGAAATGAAACCTGACCAATTAAGAAATACCA 541
QY 709 MetGluGlnTyThrArgThrGluGluGluSerAlaArgGlyIleIlePheThrIlySThrArg 728
DB 542 ATGAGCAATATATCTAGAGATGAGATGACGACGAGAAATATCTTTACAAAACAGCA 601
QY 729 GlnSerAlaTyraIaleuSerGlnTrpIleThrgluAsngluTylysPheAlaGluValGly 748
DB 602 CAGAGTCATATGCGCTTTCCAGTGATTAAGAAATGAAATTTGCTGTAAGTACGGA 661
QY 749 ValIysAlaHisIleuIleGluIleGlyAlaGlyHisSerSerGluPheTyProMetThrGln 768
DB 662 GTCMAAGCCCACTATGATGAGCTGACACAGAGATTCAAACCCATGACACAG 721
QY 769 AsngluGlnIysgluValIleSerIysPheArgThrGlyIlyserIleAsnLeuIleAla 788
DB 722 ATGAAACAAAGAAAGTCAATTGATTAATTTCCGACTGAAATAATCTGCTTATCGCT 781
QY 789 ThrThrValAlaGluGluGluTyLeuAspIleTyGluCysAsnIleValIleArgTyrgly 808
DB 782 ACCACAGTGGCAGAAAGAGTCTGATATTAAGAAATGATATCTTTATCGCTTATGCT 841
QY 809 LeuValThrAsngluIleAlaMetValGlnAlaArgGlyArgAlaArgAlaAspGluSer 828
DB 842 CTCGTGAC-AATGAATATACCATGATGCTCCAGGCCCGTGTGAGCCAGAGTGAATGAG 900
QY 829 ThrTyraIleuValAlaHisSerIysSerGlyValIleGluHisGluThr-----Val 846
DB 901 ACCTAGCTCTGCTGCTCACTGCTGCTCA-----GAGATGAACAGTGAACAT 921
QY 847 AsnAspPheArgGluTyMetMetTyTyAlaIleHisCysValGlnAsnMetTyPro 866
DB 952 AATGATTTCCGAGA-AAAGATGATGATTAAG-----CTATACATGGCGTTCAAAATGAAACCG 1007
QY 867 GluGlu 868
DB 1008 GAGGAG 1013

RESULT 6
BQ960157 870 bp mRNA linear EST 21-AUG-2002
LOCUS
DEFINITION
AGENCOURT 8949486 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6472264
5', mRNA sequence.
ACCESSION
BQ960157
VERSION
BQ960157.1 GI:22375635
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 870)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14005 row: 0 column: 17
High quality sequence stop: 738.
Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6472264"
/cissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Alignment Scores:

Pred. No.: 1, 7e-136 Length: 870
Score: 1376.00 Matches: 279
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 97.6% Mismatches: 2
Query Match: 25.9% Indels: 5
Gaps: 0

US-09-515-363c-2 (1-1025) x BQ960157 (1-870)

QY 592 LysGlyAsnArgLysGluArgValCysAlaGluHisLeuArgLysTyrAsnGluAlaLeu 611
Db 3 GAAGAAATCGCAAGACGTTGTGCGAGAAAT-TTGAGGAAGTACATGAGGCCCTA 61
QY 612 GlnIleAsnAspThrIleArgMetIleAspAlaTyrThrHisLeuGluThrPheTyrAsn 631
Db 62 CAAATTAAAGACCAATTGCATGATGATGATGCGTATATCTTGTGAACCTTCTTAAAT 121
QY 632 GluGluLysAspLysPheAlaValIleGluAspSerAspGluGlyGlyAspAsp 651
Db 122 GAAGAAAGATTAAGAAAGTTGCGAGTCATGAAGATGATGATGATGATGATGATGAT 181
QY 652 GluTyrCysAspGluAspGluAspGluAspPheLeuLysPheLeuLysLeuAspGlu 671
Db 182 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
QY 672 ThrAspArgPheLeuMetThrLeuPhePheGluAsnAsnLysMetLeuLysArgLeuAla 691
Db 242 ACGATAGATTTCTCATGACTTTATTTTGAACAATTAATGTTGAAAAGCTGGCT 301
QY 692 GluAsnProGluTyrGluAsnGluLysLeuThrLysLeuArgAsnThrIleMetGluGln 711
Db 302 GAAGAACCGAATATGAATGAAGAGCTGACCAATTAAGAAATGCAATATGAGGCA 361
QY 712 TyrThrArgThrGluGluSerAlaArgGlyIleIlePheThrLysThrArgGlnSerAla 731
Db 362 TATACTAGGACTGAGCAATCAGACAGAGAAATATCTTTACAAAACACACAGAGTGA 421
QY 732 TyrAlaLeuSerGlnTrpIleThrGluAsnGluLysPheAlaGluValGlyValLysAla 751
Db 422 TATGCCCTTTCCAGTGAGATTACTGAATAAGAAAATTTCTGAAGTGAAGTCAAAACC 481
QY 752 HisHisLeuLysLeuAlaGlyHisSerSerGluPheLysPheMetThrGlnAsnGluGln 771
Db 482 CACCATCTGATTTGGAGCTGACACAGCAGAGTCCAAACCCATGACACAGAAATGAACA 541
QY 772 LysGluValIleSerLysPheArgThrGlyLysIleAsnLeuLeuIleAlaThrTrpVal 791
Db 542 AAGGAAGTCATTTGTAATTTCCACATGCAAAAATAATTCGCTTACCGCTACACAGTG 601
QY 792 AlaGluGluGluLysLeuAspLysLeuGluCysAsnIleValIleArgTyrGlyLeuValThr 811
Db 602 GCGAAGAAAGCTTCGATATTAAAGAAATGAATTAACATTGTTATCCGTTATGCTCGTCACC 661
QY 812 AsnGluIleAlaIleMetValGlnAlaArgGlyArgAlaArgAlaAspGluSerThrTyrVal 831
Db 662 AATGAATATGCGCATTTGCTGATTTAAAGAAATGAATTAACATTGTTATCCGTTATGCTCGTCACC 721
QY 832 LeuValAlaHisSer-GlySerGlyValIleGluHisGluThrValAsnAspPheArgGly 851

Db 722 CTGCTTCTCACAGTGGCTTCAGAGTATTCGACGTCAGACGTTAATGATTTCCGAGA 781
QY 851 ulysMetMetTyrLysAlaIleHisCysValGlnAsnMet-LysProGluGluTyr--Al 870
Db 782 GAAGATGATGATTAAGCTATACATTTGTCTCAAAATATGAAGAAACAGAGGATATGGCC 841
QY 870 AhlSylvie 873
Db 842 TCATAGATT 851

RESULT 7

LOCUS CR857114 2530 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp46900632 (from clone DKFZp46900632).
ACCESSION CR857114
VERSION CR857114.1 GI:55725101
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pongo.

REFERENCE

1. (bases 1 to 2530)
Bahr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Osanger, A.,
Fobo, G., Han, M., and Wiemann, S.
The German cDNA Consortium
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann. Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
sequenced by Qagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp46900632) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp46900632
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

source
1. .2530
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp46900632"
/cissue_type="kidney"
/clone_lib="469 (synonym: pkid1). Vector pSport1_Sfi; host
DH10B; sites Sfi1A + Sfi1B"
/dev_stage="adult"
/note="hypothetical protein (Homo sapiens)"
1. .2530
/gene="DKFZp46900632"
121. .2157
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/codon_start=1
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/protein_id="CAH89418.1"
/db_xref="GI:55725102"
/translation="METLRPYQMEVIMPALEGNIIILPTGAKTRAAAYVAKRHLET
VNGKVVVLRVHLVTOHGEFRRLDGRMTTTLDSGMRPAGRGHAKRDLILC
TALDMLATSPBEHEHLETLFSLVDECHTQDTYNYVIMSGYILKIKORAPL
PVLGLTASPTGSGSKLGNATINVLQDLCANLDTWCKINSPOYTCPLQDSHSPCKQY
NCHRSQDPFDLKKLMDQIHDLMEBELSRNRTQMYEQOVVLSAAALAGLQDE
QVVYLAHLERVNDALIHDTVAVALALADOFYNEHNTKQIICAKRRLALFDDH
KNVLAHLHGPENPLBMLEKILORFSSSPSGIIFPTROSASHSLILMLQQQPG
LQTVDRADLLIGAGSSQSTHMTORDQEVIRKRPDGLNLVLVASVEEGDIDPC
NVVYRGILTNEISVQAGRARADQSYSPATRSRBLKXELINEALETGLMEQAVA
AVQKMDQAYQAKIRLDQDALTKRAQDAQRENDKQRPVEHVQLCTNCNVAVGHS
SDLRKEGTHNVNVPFSIYYNVSDPVLINKVFQDMKRGVITSCRNGCBVWGLOMI
YKSVKLPAKLVSMLETPQGRIOAKKMSRVFSPVDFDLQHCANLSDLSLD"

ORIGIN

Alignment Scores:

Pred. No.:	1.1e-134	Length:	2530
Score:	1366.00	Matches:	294
Percent Similarity:	60.3%	Conservative:	138
Best Local Similarity:	41.0%	Mismatches:	233
Query Match:	25.7%	Indels:	52
DB:	4	Gaps:	12

US-09-515-363C-2 (1-1025) x CR857114 (1-2530)

Oy	306	leuglneuaaproytgiymegluvalaaglnproalaleuugluylvsaasnlle	325
Oy	306	
Db	121	atgagagctgcgaccttaccatggaggatgatacatgctgcctcgagagggcaaaatattc	180
Oy	326	llellecybsleuprothrgliserqlyystrhrargvalalavaltyrtlealalyaasp	345
Oy	326	
Db	181	atcatcttgctgcccacacgggtgccgggaagaccggcgcgcttgcttattgtgccaaagcg	240
Oy	346	hlsleuaplyblybalybaleasergluproglylvsvallevalleuvalasnlvs	365
Db	241	cacctagag-----actgtgatgagagcaagctgtgtgtattgtgtaacacgg	288
Oy	366	valleuenuvalgluglnleupheargylsrlpheglnprophelenublyltyrtpyr	385
Db	289	gtgacactgggtgacccag---cattgtaaaagattcacggccgcatcgatgtagacgctgg	345
Oy	386	argvalilleglyleuserqlyaspthrglnleuyslleserphetrogluvalvalvs	405
Db	346	accatgaacaccttgatgtaggggacatgggacacactgctggctttggccactggccgg	405
Oy	406	sercyasapllellelleserthrallaglnlleuglnuasenserleuenuleugln	425
Db	406	tgccatgacctgctcatctatgcacggcagacttgcagatggcactgacacacgcccag	465
Oy	426	asnglylguapalaglyvalglneuserapheaserleuullellelasaglnlvs	445
Db	466	-----gagagagagacattgtagctcctctctccgtgattgtagtgaatgaagtcg	519
Oy	446	hlshtthrtaanlysgluvalavaltyrtaasnnllewecarghstytylemetglnlvs	465
Db	520	caccacacgacacagagacacgctgtcacacgctcatcattagaccagcttactgaactaaa	579
Oy	466	leuylsaanaanaargleuylblysgluasnlvsprovalleproleuproglnllelu	485
Db	580	ctccagagagacagag-----ccgcttaccacaggtgctg	612
Oy	486	glyleuthralaserproglylvalgllylathrlsrglnalalybaleuglnlhis	505
Db	613	ggtctcacagcctctccacagacatggccggcgcttccaaagctcaattggggccatcaacac	672
Oy	506	lleleuylsleucyvalaasnlleuapalaphethrilleusthrtvallysgluasnlleu	525
Db	673	gtcttcgacgctctgtggccaacttgagacagtggtgcatcattgacaccccaaaactactgc	732
Oy	526	aspglnleuylsasnglnlleglngluprocyslyslvsphaalallealaaspalathr	545
Db	733	ccccagctgcgacagacacagccaacagcttggcaaacgtaaacactctgtcacagggcc	792
Oy	546	argtluaspprophelysgluylsleuleuglnllewethrarglleglnthrttycys	565
Db	793	agcccgagatccgtttggagacttcttgaaagaaactcattgacacaaattccacagacactg	852
Oy	566	glnmetsearprometser---asphelglythrnglnprotyrglugintrpalllegl	584
Db	853	gagatgcttgacttgacccggaacttttgaaacgagatgattgacacacagctgtgaag	912
Oy	585	metglnlyblybalaalalybaleqlyasnarglysgluargvalcybalegluhlsleu	604
Db	913	ttgagtatgagcgctgctgttgccggcgctccagagacaaacgggtgtatgaccttcacctg	972
Oy	605	arglysttyraenglualeuglnlleasnaapthrtlleargmetlleaspalatyrthr	624
Db	973	agggccttcaatgacgcctgctctcatcattgacacacgctgcgcgcgttggaatgcttgctt	1032

QY	625	HisLeuGIuThrPheTyrrAsnGIuGluLysAspIyLePheAlaValIleGluAsp	644
Db	1033	GCGCTGACGAGATTTCATCACAGGAGCAGATCTCACTAAACCCAGATCTG----	10833
QY	645	SerAspGIuGIyGIAspAspGIuTy-CysAspGIyAspGIuAspGIuAspAspLeuIys	664
Db	1084	-----TGT-----	1086
QY	665	LysProLeuIyIAspAspGIuThrAspArgPheLeuMetThrLeuPhePheGluAsnAsn	684
Db	1087	-----GCCAAGGCGCGGTGCTGGCCCTGTTCGATGACCAAG	1125
QY	685	LysMetLeuIyIAspGluAlaGluAsnProGIuTyGIuLysGluIyIAspThrIyIAspLeu	704
Db	1126	AATGGCTGGCGCCACTGGCAACTCATGAGCCCA--GAGATTCAAAACCTGAGATGCTG	1182
QY	705	ArgAsnThrIleMetGIuGluIyThrThyArgThrGIuGluSerAlaArgGIyIleIlePhe	724
Db	1183	GAAAAGATCTCGCAAGGAGCTTC--AGGAGCTTGACACCTCGGGGATATCATCTTC	1239
QY	725	ThyIyThrArgIuSerAlaTyAlaLeuSerGIuThrIleThrGIuAsnGIuIyAspHe	744
Db	1240	ACCGGACCGCGCAGAGGACACACTCCCTCGTGTGGCTCCAGACAGACAGCGGCTG	1299
QY	745	AlaGluValGIyValIyValAlaHisIleIleuIleGlyAlaGlyHisSerSerGIuPheIys	764
Db	1300	CAGACCGTGGACATTCGGGCGCCAGCTCATGTATGGGCTGGGAACAGACGCAAGCACACC	1359
QY	765	ProMetThrGIuAsnGIuGluIyValIleSerIyAspAspGIuThyGIyIleAsn	784
Db	1360	CACATGACCCAGAGGACACAGAAATGATCCGAGATGCCAGATGGAACCTGAC	1419
QY	785	LeuLeuIleAlaThrThrValAlaGluGIuIyLeuAspIleIySGluCysAsnIleVal	804
Db	1420	CTTCGTGGGCGCAGAGTGTGGGAGGAGGCGTGACATCCACATTCGATGTGGTG	1479
QY	805	IleArgTyGIyLeuValThrAsnGIuIleAlaMetValGlnAlaArgGIyValAlaArg	824
Db	1480	GTGCGTATGGGCTCTCGACCAATGAATCTCCATGTGCCAGGCGAGGGCGGTGCCGG	1539
QY	825	AlaAspGIuSerThrTyrrValLeuValAlaHisSerGIySerGIyValIleGluHisGIu	844
Db	1540	GCCGATCAGAGTGTACTCGTTGTGACCACTGAGGTACCGGAGCTAAGCGGGAG	1599
QY	845	ThrValAsnAspPheArgGIuIyLeuMetMetTyrrAlaIleHisCysValGIuAsnMet	864
Db	1600	CTGATCAACAGGGCGGTGAGACCGCTGATGAGCAGCAGTGGCTGTGTCAAAATG	1655
QY	865	LysProGIuGIuTyrrAlaHisIyIleLeuGIuLeuGluMetGlnSerIleMetGIuIy	884
Db	1660	GACCAAGCTGATACAGCCAGCAAGTCCGGGATCTGACGAGCGACCTGACCAAGCGG	1719
QY	885	LysMetIyThrIyIAspAsnIleAlaIyHisTyrrIyAsnAsnProSerLeuIleThr	904
Db	1720	GCGGCGCAGGAGCCACAGCGGAGAACAGCGGCGGAGTTCCAGTGGACACGTGAG	1779
QY	905	PheLeuCysIyAsnCysSerValIleuAlaCysSerGIuAspIleHisValIleGIu	924
Db	1780	CTACTCTCATCACTGATGATGGCGGTGGCGCCAGCGACACACTGCGGAAGTGGAG	1839
QY	925	LysMetHisIleValAsnMetThrProGIuPheIySGluLeuTyrr--IleValArgGIu	943
Db	1840	GGCACCCAGCAATGTCAACGTGACCCCGCTTCGATCTCACTAATATGTCTCCAGGGAT	1899
QY	944	AsnIyValaLeuGIuIyIyCysAlaAspTyrrGlnIleAsnGIuIleIleCysIyIys	963
Db	1900	CCTGTGTCATCAACAAAGCTTTCAGAGACTGGAGCGCTGGGGGTGCATAGCTGCAGG	1955
QY	964	---CysGIuIleAlaTyrrGIyThrMetMetValHisIySGluIyAspLeuProCysLeu	982
Db	1960	AACGTGGGAGGCTGTGGGCTCTGCAGATGATCTCAACAGTCAAGTGAAGCTGCCAGCGCTC	2019
QY	983	LysIleArgAsnPheValValIlePheIyAsnAsnSerThrIyIySGluTyrrIyIyIy	1002


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Db      2020 AAGATCCGAGC-----ATGCTGCTGAGAGACCCCTCAGGGGGGATCCAGGCAAAAG 2073
Qy      1003 TTPValGluLeuProIleThrPheProAlaLeuAspTyrSerGluCys 1019
Db      2074 TGGTCCCGGGTCCCTTCCTCCGCTGCTGACTTGAATCTCTGAGACATTGT 2124

RESULT 8
LOCUS   BU189982
DEFINITION AGENCOURT_7950921 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6173848
5' mRNA sequence.
ACCESSION BU189982
VERSION   BU189982.1 GI:22703966
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 918)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsabers-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13546 row: a column: 17
High quality sequence stop: 556.
Location/Qualifiers
1. 918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6173848"
/feature_type="leiomycarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NIH_MGC_71"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb. "

ORIGIN
Alignment Scores:
Pred. No.: 3.64e-127 Length: 918
Score: 1289.50 Matches: 269
Percent Similarity: 95.1% Conservative: 5
Best Local Similarity: 93.4% Mismatches: 6
Query Match: 24.3% Indels: 8
DB: 5 Gaps: 1

US-09-515-363c-2 (1-1025) x BU189982 (1-918)

Qy      360 TLevalLeuValAsnLysValLeuLeuValGluGlnLeuPheArgLysGluPheGlnPro 379
Db      2 ATATGTTCTTGTCAATAAGGACTGCTAGTGAACACTCTTCGCAAGGAGTTCCAAACCA 61
Qy      380 PheLeuLysLysTrpYrArGValIleGlyLeuSerGlyAspThrGlnLeuLysIleSer 399
Db      62 TTTTAAAGAAAGGATCGTCTGTTATGATTAAGTGATACCCCACTGAAATAATATCA 121
Qy      400 PheProGluValValLysSerCysAspIleIleIleSerThrAlaGlnIleLeuGluAsn 419
Db      122 TTTCAGAAAGTTGTCAAGTCTCTGTATATTATATACGATCAAGCTCAAACTCTTGAAGC 181
Qy      420 SerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeu 439

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Db      182 TCCCTTTAACTTGGAATAATGAGAAAGATGCTGCTTCAATTGTCAAGCTTTCCCTC 241
Qy      440 TLeIleIleAspGluCysHisIleThrAsnLysGluAlaValTyrAsnAsnIleMetArg 459
Db      242 ATTATCATTTGATGATGATCATACACCAACAAAGAGAGGTGTATATATATCAATCAAGG 301
Qy      460 HisTyrLeuMetGlnLysLysLysAsnAsnArgLysLysGluAsnLysProValIle 479
Db      302 CATTAATTGATGACAAAGTTGAAAAACAATACACTCAAGAAAGAAACCAACACAGATT 361
Qy      480 ProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGlyValAlaThrLysGln 499
Db      362 CCCCTTCTCAGATACCTGGAGCTTAACAGCTTCACTCGTGTGGAGGGCCACGAAGCA 421
Qy      500 AlaLysValGluGlnHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThrIleLys 519
Db      422 GCCAAAGCTGAAGAACACTTTTAAACTATGTGCCAATCTTGATGCAATTTACTATTAA 481
Qy      520 ThrValLysGluAsnLeuAspGlnLeuLysAsnGlnIleGlnGluProCysLysLysPhe 539
Db      482 ACTGTTAAAGAAACCTTGATCACTGAAACCAAAATACAGAGCCATGCAAGAGTT 541
Qy      540 AlaIleAlaAspAlaThrArgLysAspProPheLysGluLysLeuLeuGlnIleMetThr 559
Db      542 GCCATTCAGATGCACCAACGAGAAAGATCCATTTAAAGACAACTTCAAAATAATAGCA 601
Qy      560 ArgIleGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGlu 579
Db      602 AGGATTCAAACTTATATGTCAAATGAGTCCAAATGTCAGATTTGGAACTCAACCTATGAA 661
Qy      580 GlnTPala---IleGlnMetLysLysValAlaLysLysGlyAsnArgLysGluArg 598
Db      662 ACATGGCCCATTCCAATGCAAAAAAGCCCTGCAGAAAGAAATGCAAGAAAGCT 721
Qy      599 Val-CysAlaGlnHisLeuArgLysTyrAsnGlu-AlaLeuGlnIle-AsnAspThrIle 617
Db      722 GTTTGTGCAAAACATTGAGAGAGTACATGAAGCCCTTACAAATAATGACCAAT 781
Qy      618 ArgMet-IleAspAlaTyrThrHisLeu-GluThrPheTyrAsn-GluGluLysAsp-Ly 636
Db      782 TCATGATGAATTAATGCTATATCATCTTGAACCTTCTATATATGAGAAAGATTAG 841
Qy      636 GlyPhePala 639
Db      842 AAGATTTCGC 851

RESULT 9
LOCUS   BU902097
DEFINITION AGENCOURT_10127740 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6502757
5' mRNA sequence.
ACCESSION BU902097
VERSION   BU902097.1 GI:24084010
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsabers-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14059 row: f column: 06

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FEATURES
High quality sequence stop: 808.
Location/Qualifiers
1. 1174
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5532884"
/issue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6, Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.1 kb."

ORIGIN

Alignment Scores:
Pred. No.: 1.67e-123 Length: 1174
Score: 1257.00 Matches: 271
Percent Similarity: 87.8% Conservative: 10
Best Local Similarity: 84.7% Mismatches: 19
Query Match: 23.7% Indels: 20
DB: Gaps: 1

US-09-515-363C-2 (1-1025) x BU902097 (1-1174)

QY 1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuLysSerCysPheArgAla 20
DB 223 ATGTCCAAAGGGATATTCACAGACGAAATTCGGCTATCTCATCTCGAGCTTCAGAGGCC 282
QY 21 ArgValIleMetTyrIleGlnValGluProValIleuAspTyrLeuThrPheLeuProAla 40
DB 283 AGGGTAAATATGATACATCCAGGTGAGACCTGTGCTGAGACTGACCTTTCGGCTGCA 342
QY 41 GluValIleGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60
DB 343 GAGGTAGAGAGCAGATTGACAGACAGATCCGACCTCCGGAAACATGACGAGCTTGAA 402
QY 61 LeuLeuLeuSerThrLeuGluGluValIleThrIleLeuGlyTyrThrArgGluPheVal 80
DB 403 CTGCTCTGACACCTTGAGAAAGGAGTGTGACCTTGAGTGTGACTCGGAAATTCG 462
QY 81 GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100
DB 463 GAGGCCCTCCGAGAACCCGACCTCTGCGCCCGCTACATGAACCTGAGCTCAG 522
QY 101 AsnLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeu 120
DB 523 GACTGCCCTCTCATCTGTTGAGAACGCTCATGATGATATCTCCAACTGCTGAACCTC 582
QY 121 LeuGlnProThrLeuValAspIleLeuValArgAspValLeuAspIleCysMetGlu 140
DB 583 CTTCACCCCACTGTGTGACAAAGCTTCTATGAGACCTCTTGATTAAGTCTCATGAG 642
QY 141 GluGluLeuLeuThrIleGluAspArgAsnArgIleAlaAlaIleGluAsnAsnGlyAsn 160
DB 643 GAGGAAGCTGTGCAATTGAAAGACAGAAACCGGATTCCTCTCAGAAAAACATGAAAT 702
QY 161 GluSerGlyValArgGluLeuLeuLeuValIleValGlnIleGluAsnTrpPheSerAla 180
DB 703 GAATCAGGTGTAGAGAGCTACTAAAGAGATTGTCCAGAAAGAAATCGTCTCTGCA 762
QY 181 PheLeuAsnValLeuArgGlnThrGlyAsnAsnGluLeuValGlnIleLeuThrGlySer 200
DB 763 TTTCTGAAGTCTTCTGCTCAACAGAAACAAAGAACTGTCACAGAGTTAAAGAGCTCT 822
QY 201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220
DB 823 GATGCTCAGAAAGCAATGACAGATTGAGAAATTTATCAACAATTGATGCTCTCAAGTC 882
QY 221 -GluGlnIleLeuLeuSerThrThr-ValGlnProAsnLeuGlu-LysGluValITPGLY 239
DB 883 GGAAAGCAACTCTTTCAACACACAGGTTCAAGCAATCTGAAAAAGAGAGTCTGGGCG 942

QY 240 MetGlu-AsnAsnSerSer-GluSerSerPheAlaAspSerSerValValSerGluSer 259
DB 943 ATGGAAAAATTAATCTATCAAAAATCATCTTTGACAGATCTTCTGAAGTTCCAGAACCA 1002
QY 259 spThrSerLeuAla-GluGlySerValSerCysLeu-AspGluSer-LeuGlyHisAsn 278
DB 1003 AACCAAGTTGGCCAAAGAAAGAAATGCACTCTTAATGAAGCTTGGGACATMAACA 1062
QY 278 ArgAsnMetGlySerAsp-----SerGlyT 286
DB 1063 ACAACATGGGCGAGGATTTCCGGCCCCCGGGCCAAAGATTTCAAATATAAAAAAGGG 1122
QY 286 hMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300
DB 1123 CCACCAAGAAATATCCCGGAAACAAAAATTCAGCTTGGGCG 1166

RESULT 10
BM467983 1115 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT 6437921 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532884
DEFINITION 5', mRNA sequence.
ACCESSION BM467983 GI:18517025
VERSION BM467983
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1115)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12216 row: n column: 21
High quality sequence stop: 690.

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5532884"
/issue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6, Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.1 kb."

ORIGIN

Alignment Scores:
Pred. No.: 2.39e-119 Length: 1115
Score: 1218.00 Matches: 228
Percent Similarity: 99.1% Conservative: 0
Best Local Similarity: 99.1% Mismatches: 2
Query Match: 22.9% Indels: 0
DB: Gaps: 0

US-09-515-363C-2 (1-1025) x BM467983 (1-1115)

QY 796 LeuAspIleLeuGluCysAsnIleValIleArgTyrGlyLeuValThrAsnGluIleAla 815
DB 1 TTGGATATTAAAGAAATGTAACATTTGATCCGTATGCTGTCACCAATGAATAAGCC 60
QY 816 MetValGlnAlaArgGlyArgAlaArgAlaAspGluSerThrTyrValLeuValAlaHis 835

|||||
61 ATGTCACGCGCCGCTGCTGAGCCAGAGCTGATGAGACGACCTACCTCTGCTGCTGCTAC 120
QY 836 SerGlySerGlyValIleGluHisGluThrValAsnAspPheArgGluLysMetMetYr 855
Db 121 AGTGGTTCAGAGGATTAACGACCTGACAGAGTTAAATGATTTCCGAGAGAAAGATGATTA 180
QY 856 LysAlaIleHisCysValGlnAsnMetLysProGluGluTyrLanHisLysIleLeuGlu 875
Db 181 AAGCATATCATTTGCTTCAAAATATGAAACGAGAGATGCTCATAGATTTTGGAA 240
QY 876 LeuGlnMetGlnSerIleMetGluLysLysMetLysThrLysArgAsnIleAlaLysHis 895
Db 241 TTACAGATCCAAAGTAAATGAGAAAAGAAAATGAAAACGAGAAATATTTGCCAAGCAT 300
QY 896 TyrLysAsnAsnProSerLeuIleThrPheLeuCysLysAsnCysSerValIleuAlaCys 915
Db 301 TACAGAAATTAACCATCACTAAATTAATCTTCTTGGAAAACCTGCAGTGTGCTAGCCTGT 360
QY 916 SerGlyGluAspIleHisValIleGluLysMetHisHisValAsnMetThrProGluPhe 935
Db 361 TCTGGGGAAGATATCATGATTAATGAGAAATGCAATGCAATGATGACCCAGAAATTC 420
QY 936 LysGluLeuTyrIleValIArgGluAsnLysAlaLeuGlnLysLysCysAlaAspTyrGln 955
Db 421 AAGGAATTTACATTTGTAAGAGAAAACAAACACCTGCAAAAGAAAGTGTCCGACTATCAA 480
QY 956 IleAsnGlyGluIleIleCysLysCysGlyGlnAlaIleThrGlyThrMetMetValHisLys 975
Db 481 ATTAATATGTAATCACTGCAAAATGTGGCAGGCTTGGGGAACAAATGATGTGCACAA 540
QY 976 GlyLeuAspLeuProCysLeuLysIleArgAsnPheValValPheLysAsnAsnSer 995
Db 541 GCGTTATGATTTGCTGCTGCTCAAAATTAAGGAATTTGTAGTGTGTTTCAAAAATATTC 600
QY 996 ThrLysLysGlnTyrLysLysTyrValIleGluLeuProIleThrPheProAsnLeuAspTyr 1015
Db 601 ACAAGAAACAAATACAAAAGTGGGTAGAAATTAATCAATCAATTTCCCAATCTTGACTAT 660
QY 1016 SerGluCysCysLeuPheSerAspGluAsp 1025
Db 661 TCAGAAATGCTGTTATTATTAATGATGAGAGAT 690
RESULT 11
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LOCUS BF337464
DEFINITION 602035195F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183126
5' mRNA sequence.
ACCESSION BF337464
VERSION BF337464.1 GI:11283715
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1035)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHM9498 row: n column: 23
High quality sequence start: 5
High quality sequence stop: 695.
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4183126"
/feature_type="glcloblastoma with EGFR amplification"
/lab_host="DH10B (TI phase-resistant)"
/clone_11b="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NCI;
Site 2: Salt; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 3,65e-118 Length: 1035
Score: 1206.50 Matches: 264
Percent Similarity: 84.0% Conservative: 15
Best Local Similarity: 79.5% Mismatches: 44
Query Match: 22.7% Indels: 12
DB: Gaps: 5
US-09-515-363c-2 (1-1025) x BF337464 (1-1035)
QY 295 AasnValAlaAlaArgAlaSerProGluProGluLeuGlnLeuArgProTyrGlnMetGlu 314
Db 6 AATGTGGCAGCAAGAGCATCCCGGAGCCAGAACTCCAGCTCAGGCTTACCAAAATGGAA 65
QY 315 ValAlaGlnProAlaLeuGluGluLysAsnIleIleCysLeuProThrGlySerGly 334
Db 66 GTTGGCCAGCCAGCCTTGGAGGAGAAATATCATCATCTGCTCTACAGGAGTGGA 125
QY 335 LysThrArgValAlaValTyrIleAlaLysAspHisLeuAspLysLysLysLysAsp 354
Db 126 AAAACCAAGTGGCTGTTTACATTCACCAAGATCACTTAAGACAGAGAAAACATCT 185
QY 355 GluProGlyLysValIleValIleuValAsnLysValLeuLeuValGluGlnLeuPheArg 374
Db 186 GAGCTCGGAAAAGTTATAGTCTTCTCAATAAGTACTGCTAGTGAACAGCTCTTCCGC 245
QY 375 LysGluPheGlnProPheLeuLysLysTyrTyrArgValIleGlyLeuSerGlyAspThr 394
Db 246 AAGGAGTTCACACATTTTGAAGAAATGTAATCGTGTATTAGATTAATAGTGATAC 305
QY 395 GlnLeuLysIleSerPheProGluValValLysSerCysAspIleIleIleSerThrala 414
Db 306 CAATGAAATATCATTTCTCAGAGTGTCAAGTCTCTGTGATATTAATATCAGTACAGCT 365
QY 415 GlnIleLeuGluAsnSerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeu 434
Db 366 CAATCTCTGAAAACTCCCTCTTAAACTTGAATAATGGAAGATGCTGTCTCAATTG 425
QY 435 SerAspPheSerLeuIleIleIleAspGluCysHisHisThrAsnLysGluAlaValTyr 454
Db 426 TCAGACTTTTCCCTCATTTATCATTTGATGATATCTACACACAAAGAACAGATGAT 485
QY 455 AasnAsnIleMetArgHisTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysGlu 474
Db 486 AATTAATCATATGAGCATATTATGATGCAAGATTGAAAACAAATATGACTCAAGAAAGA 545
QY 475 AasnLysProValIleProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGly 494
Db 546 AACCAACCAAGTATTCCTCTCTCAGATACAGGACATCAAGCTTCACTGTGTCCGA 605
QY 495 GlyAlaThrLysGlnAlaAlaValIleGluGlnHisIleLeuLysLeuCysAlaAsnLeuAsp 514
Db 606 GGAGCCACAGAACCAAGCCAAACCTGAAGAACCATTTTAAACTATGTGCCAATCT-GAT 664
QY 515 AlaPheThrIleLysThrValLysGluLeuLeuAspGlnLeuLysAsnGlnIleGlnGlu 534
Db 665 GCATTTTACTATTAATCTGTGAAGAAAACCTTGATCACTGGGAAAACCAATATCAGAG 724
QY 535 ProCysLysLysPheAlaIleAlaAspAlaThrArgGluAspProPheLysGluLysLeu 554

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Db      725 CCATCGGAGAAAGTTGGCGCT-GCGGATGCGAC-CGAGAAGATCCCTTTAAGGGAAC--- 779
Qy      555 LeuGluIleMetThrArgIleGlnThrTyArgGlnMetSerPro-MetSerAspHeG 574
Db      780 ---TCTGAATAATAGCAGGGGTTCCACTTGTGTGAGT---AGTCCAGGTCCA---TTGGG 830
Qy      574 yThrgInProTyrgLgInTrpAlaIleGlnMetGluLysLysAlaAlaLysLysGlyAs 594
Db      831 TACCCACCCCTATTAA-----GGGCGCTCAACGGGGGAAAGGGGCTTAGAAGCAAA 884
Qy      594 nArgLysGluArgValCysAlaGluHisLeuArgLysTyArgnGluAlaLeuGlnIleAs 614
Db      885 ACGGTTGGCGACCTTGGGGCGAACAAGCGCACAAAGAGACACAGAAAGGCGACACAA 944
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RESULT 12
LOCUS   DR422160                690 bp    mRNA    linear    EST 29-JUN-2005
DEFINITION   nav08g05.y1 Human pterygium. Unnormalized (nav) Homo sapiens cDNA
ACCESSION   DR422160
VERSION     DR422160.1    GI:68324176
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 690)
            Wistow,G., Jaworski,C., Aryankalayil-John,M., Rowsey,J.J., Cox,C.,
            Reid,T., Dushku,N. and Carper, D.
            NEIBank analysis of Human pterygium
            Unpublished (2005)
            Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 08 row: 9 column: 05
            Seq primer: Universal M13 Reverse.
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                     /dev_stage="Adult"
                     /lab_host="EMDH108"
                     /clone_lib="Human pterygium. Unnormalized (nav)"
                     /note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted
                     from 9 pooled human pterygia. A directionally cloned cDNA
                     library in the pCMVSPORT6 vector (Invitrogen) was
                     constructed at Bioserve Biotechnology (Laurel MD)
                     essentially following the protocols of the Superscript
                     Plasmid System, full details of which are contained in the
                     manufacturer's instruction manual
                     (http://www.lifetech.com/). First strand synthesis was
                     carried out using a Not I primer-adaptor
                     [5'-PGACTAGTCTAGATCGACGCGCGCCCT(T)15-3']. cDNA was
                     cloned in Not I/Sal I sites. EST analysis was performed at
                     the NIH Intramural Sequencing Center (MISC). Analyzed data
                     available through http://neibank.nih.gov."
ORIGIN
Alignment Scores:
Pred. No.:          3.06e-116          Length:          690

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Score:          1186.00          Matches:          226
Percent Similarity: 99.1%          Conservative: 1
Best Local Similarity: 98.7%          Mismatches: 2
Query Match:      22.3%          Indels: 0
DB:               8          Gaps: 0

US-09-515-363c-2 (1-1025) x DR422160 (1-690)
Qy      563 ThrTyArgGlnMetSerProMetSerAspPheGlyThrgInProTyrgLgInTrpAla 582
Db      2 ACTTATGTCCTTATGTCCAATGTCAGATTGTGAATCTAACCTTAGAACAATGGCC 61
Qy      583 lLgInMetGluLysLysAlaAlaLysLysGlyAsnArgLysGluArgValCysAlaGlu 602
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Qy      603 HisLeuArgLysTyArgnGluAlaLeuGlnIleAsnAspThrIleArgMetIleAspAla 622
Db      122 CATTGAGGAGAGACAAATAGAGCCCTTACAAATTAATGACACAAATTCGAATGATGATCG 181
Qy      623 TyThrHisLeuGlnThrPheTyArgnGluLysLysLysLysPheAlaValIleGlu 642
Db      182 TATACATCATCTTGAAACTTTCTATTAATGAAGAAGAAATGATGAAGTTGCATGAGAA 241
Qy      643 AspAspSerAspGluGlyGlyAspAspGluTyTyCysAspGlyAspGluAspGluAspAsp 662
Db      242 GATGATAGTGAAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
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Db      362 AACCAATAAATGTTGAAAAGGCTGGCTGAAAACCCGAATATGAATAATAAAGCTGACC 421
Qy      703 LysLeuArgAsnThrIleMetGluGlnTyTrgArgTrgGluGluSerAlaArgGlyIle 722
Db      422 AATTTAGAATAATCCATTAATGAGCAATTAATGAGATGAGCAATGAGCAATGAGCAAT 481
Qy      723 lIlePheThrLysThrArgGlnSerAlaTyAlaLeuSerGlnTrpIleThrgLysGlu 742
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Qy      743 LysPheAlaGluValGlyValLysAlaHisIleLeuIleGlyAlaGlyHisSerSerGlu 762
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Qy      763 PheLysProMetThrgLysnGluGlnLysGluValIleSerLysPheArgThrgLys 782
Db      602 TTCAAACCATGACACAGAAATGACAAAAGAAATGATTAATTTGGCACTGAAAAA 661
Qy      783 lIleAsnLeuLeuIleAlaThrVal 791
Db      662 ATAAATCTGCTTATCGCTACACAGTG 688

RESULT 13
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ACCESSION   BF983236
VERSION     BF983236.1    GI:12386048
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 729)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)

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COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9abbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>
 Plate: L14M10097 row: a column: 20
 High quality sequence stop: 665.
 Location/Qualifiers

FEATURES

source

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 /clone="IMAGE:4397083"
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 /clone_1b="NIH MGC 88"
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 site 1: NotI; site 2: SalI; Cloned unidirectionally;
 oligo-dt primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,44e-110 Length: 729
 Score: 1129.00 Matches: 238
 Percent Similarity: 98.4% Conservative: 4
 Best Local Similarity: 97.5% Mismatches: 3
 Query Match: 21.3% Gaps: 0

US-09-515-363C-2 (1-1025) x BF983236 (1-729)

QY 140 GUGUGUGUleuLeuThrlleGUAePArGAsnArgileAlaAlaAGluAsnAngly 159
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 DB 181 TCTGATGTCTCAAGAAAGCAATGAGATTGAGATTATTCACAAAGTTGATGCTCTCA 240
 QY 220 ValGluGluGluLeuLeuSerThrValGlnProAsnLeuGluLyGluValITrpgly 239
 DB 241 GTGGAGAGCAACCTTCTTCAACACAGCTTCAGCCAAATCTGGAGAGAGGCTCTGGGG 300
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 DB 361 ACAAGTTTGGCAGAGAGAGAGTGTACACTGTTTGAAGAAAGCTTGGACACTTAACAGAAC 420
 QY 280 MetGlySerAaSpSerGlyThrMetGlySerAaSpSerAaSpGluGluAsnValAlaAlaArg 299
 DB 421 ATGGCAGAGGATTCAGGACCAATGAGAGAGATTCAGATGAGAGATGTGGCAGCAAG 480
 QY 300 AlaSerProGluProGluLeuGlnInLeuAArgProGlyGlnMetGlyValAlaGlnProAla 319
 DB 481 GGATCCCGAGAGCAGAACTCCAGCTCAGGCTTACCAATGAGAGAGTTGCCAGCAGCAGC- 539

QY 320 LeuGluGlyLybAsnAllelleleCybLeuProThrTrgLySerGlyLybThrArgValAla 339
 DB 540 TTGAGAGGAGAGAAATATCATCTATCTGCTC-CCTACAGGAGAGGAGAAACCAAGAGTGGCT 598
 QY 340 ValTyrTleAlaLybAspHisLeuAspLybLybLybAlaSerGluProGlyLybVal 359
 DB 599 GTTTCATTTGCCAGAGATCATCTTAACAG-AGGAAAAAGCATCTGAGCTTGAAAAAGTT 657
 QY 360 lleValleuValAsnLybValleuValleuValGluGlnLeuPheArgLybGluPheGlnPro 379
 DB 658 ATATGTTCTTGTGCATATAGGTAAGTCTGCTAGTTGAACAGCTCTCCGAAAGAGATCCACCA 717
 QY 380 PheLeuLybLyb 383
 DB 718 TTTTGGAGCAAG 729

RESULT 14

BY720783

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 972)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

Mus musculus

Mus musculus (house mouse)

EST.

BY720783.1 GI:27133900

EST.

BY720783

CDNA clone 9130009C22 5', mRNA sequence.

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CDNA clone 9130009C22 5', mRNA sequence.

JOURNAL

PUBLISHED

COMMENT

CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9226
 Email: genome-research.riken.jp, URL: <http://genome-gsc.riken.jp/>
 Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F.,
 Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,

Qy	1022	SerAspGluAsp	1025
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Search completed: March 13, 2006, 21:29:16
Job time : 9431 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2006, 04:58:35 ; Search time 688 Seconds
(without alignments)
2648.257 Million cell updates/sec

Title: US-09-515-363c-2

Perfect score: 5311

Sequence: 1 MSGXSTDBNFRYLISCFRA.....LPITFPLNDYSECLFSDSD 1025

Scoring table: BLOSUM62

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Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
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Searched: 1303057 segs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1352	25.5	2590	3	US-09-799-451-771 Sequence 771, Appl
3	498	9.4	458	3	US-09-907-907A-32 Sequence 32, Appl
4	472	8.9	301	2	US-08-143-576-7 Sequence 12, Appl
5	472	8.9	301	3	US-09-221-268D-12 Sequence 12, Appl
6	406	7.6	6184	3	US-09-590-968B-1 Sequence 1, Appl
7	392.5	7.4	1664976	3	US-08-916-421B-1 Sequence 1, Appl
8	392.5	7.4	1664976	3	US-09-692-570-1 Sequence 1, Appl
9	335.5	6.3	7037	3	US-09-853-768-3 Sequence 3, Appl

10	289.5	5.5	1512	3	US-09-408-020-65 Sequence 65, Appl
11	289.5	5.5	3298	3	US-09-408-020-1 Sequence 1, Appl
12	284	5.3	1509	3	US-09-408-020-33 Sequence 33, Appl
13	284	5.3	42432	3	US-09-408-020-2 Sequence 2, Appl
14	283.5	5.3	2354	3	US-10-104-047-1641 Sequence 1641, Ap
15	227.5	4.3	193	2	US-08-143-576-6 Sequence 6, Appl
16	227.5	4.3	193	3	US-09-221-268D-11 Sequence 11, Appl
17	217.5	4.1	8257	3	US-09-595-684B-30 Sequence 30, Appl
18	212	4.0	5852	3	US-09-853-768-10 Sequence 10, Appl
19	211.5	4.0	8803	3	US-09-620-312D-130 Sequence 130, Ap
20	207.5	3.9	6773	3	US-09-166-350-27 Sequence 27, Appl
21	200	3.8	12214	3	US-09-949-016-17284 Sequence 17284, A
22	199.5	3.8	4688	2	US-08-139-937-12 Sequence 12, Appl
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27	193.5	3.6	1986	3	US-09-107-532A-23 Sequence 23, Appl
28	193.5	3.6	8590	3	US-09-949-016-5562 Sequence 5562, Ap
29	191.5	3.6	10136	2	US-08-353-700-2 Sequence 2, Appl
30	191.5	3.6	10136	6	PCT-US95-16216-2 Sequence 2, Appl
31	190.5	3.6	38575	3	US-09-949-016-17304 Sequence 17304, A
32	190.5	3.6	119153	3	US-09-949-016-12378 Sequence 12378, A
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34	188.5	3.5	4848	3	US-09-976-594-295 Sequence 295, App
35	187.5	3.5	6921	3	US-09-643-597-117 Sequence 117, App
36	187.5	3.5	6921	3	US-09-480-884A-117 Sequence 117, App
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38	187.5	3.5	6921	3	US-09-606-421B-117 Sequence 117, App
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40	187.5	3.5	6921	3	US-09-466-396A-117 Sequence 117, App
41	187.5	3.5	6921	3	US-09-476-496A-117 Sequence 117, App
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43	187.5	3.5	6921	3	US-09-285-479-117 Sequence 117, App
44	187.5	3.5	6921	3	US-10-007-700-117 Sequence 117, App
45	187.5	3.5	7045	3	US-09-919-172-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-023-655-48
; Sequence 48, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.


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; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (190)..(2223)
; US-09-799-451-771
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Alignment Scores:

Pred. No.:	5,176-139	Length:	2,550
Score:	1,152.00	Matches:	292
Percent Similarity:	59.7%	Conservative:	136
Best Local Similarity:	40.7%	Mismatches:	237
Query Match:	25.5%	Indels:	12
DB:	3	Gaps:	12

US-09-515-363C-2 (1-1025) x US-09-799-451-771 (1-2590)

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Qy	326	IleIleCysLeuProThrGlySerGlyLysThrArgValAlaValTyrIleAlaLysAsp	345
Db	250	ATCATCTGGCTGCCACGGGTGCCGGGAAGACCCGGCGGCTGCTTATGTGGCCAAACGG	309
Qy	346	HisLeuAspLysLysLysAlaSerGluProGlyLysValIleValLeuValaunLys	365
Db	310	CACCTAGAG-----ACTGTGAGTGGAGCCAAAGTGGTGTATTTGATGTCACACAG	357
Qy	366	ValLeuLeuValGluGlnLeuPheArgLysGluPheGlnProPheLeuLysIleTyr	385
Db	358	GTGACACCTGGTATCCAG--CATGTGTAAAGTTTAAAGCGCATGCTGATGGACCGCTGG	414
Qy	386	ArgValIleGlyLeuSerGlyAspThrGlnLeuLysIleSerPheProGluValValys	405
Db	415	ACCGTGACAAACCTGTAGTGGGACATGGGACACCGTGGCTTGCCACCTGGCCCG	474
Qy	406	SerCysAspIleIleIleSerThrAlaGlnIleLeuGlnAsnSerLeuLeuAsnLeuGlu	425
Db	475	TGCCATGACCTGCTCATCTGACACAGAGCCTTCTGCAATGGACACTGACACACCCGAG	534
Qy	426	AsnGlyIuAspAlaGlyValGlnLeuSerAspPheSerLeuIleIleAspGluCys	445
Db	535	-----GAGGAGGAGACGCTGGAGCTCACTGTCCTTCTCCTGATCGTGGATGAGTGC	588
Qy	446	HisIleThrAspLysGluAlaValTyrAsnAsnIleMetArgHisTyrLeuMetGlnLys	465
Db	589	CACCAACGCAAGAGACCGCTCTACAAACGTCATCATGAGCCAGTAACTAGAACTTTAA	648
Qy	466	LeuLysAsnAsnArgLeuLysLysGluAsnLysProValIleProLeuProGlnIleLeu	485
Db	649	CTCCGAGAGGCGCAG-----CCGCTACCCCGAGGTCG	681
Qy	486	GlyLeuThrAlaSerProGlyValGlyGlyAlaThrLysGlnAlaLysAlaGluGluHis	505
Db	682	GGTCTCAACAGCTCCCCCGAGCACTGGCGGGGCTCCAAACTCGATGGGGCCATCAACAC	741
Qy	506	IleLeuLysLeuCysAlaAsnLeuAspAlaPheThrIleLysThrValLysGluAsnLeu	525
Db	742	GTCTCGACAGCTGTGGCCAACTTGAGCAGTGGTGATCATGACACCCCGAAGCTGTGC	801
Qy	526	AspGlnLeuLysAsnGlnIleGlnGluProCysLysLysPheAlaIleAlaAspAlaThr	545
Db	802	CCCCAGCTGACAGAGACACGCAACGACCTTGCAACAGATCAACCTGTGCCACAGGCC	861
Qy	546	ArgGluAspProPheLysGluLysLeuLeuGlnIleMetThrArgIleGlnThrTyrCys	565
Db	862	AGCCAGAGATCCCTTTGGGACTCTGCGAAGAGCTATGAGCAAAATTCATGACCACTG	921
Qy	566	GlnMetSerProMetSer--AspPheGlyThrGlnProTyrGlnGlnTrpAlaIleGln	584
Db	922	GAGATGCTGATTTAGCCGGAATTTTGGAGCGCAATATATATAGCAGAGCTGTGGAAG	981

QY	555	metGluValblybAlaAlaIblybGlybAsnArgbysbGluabArgValbCybAlaGluHibLeu	604
Db	982	CTGATGAGGCTGGCGGCTTTGGCTGGCGGCTTACAGAGCAACGGGAGTATGGCCCTTCACTG	1041
QY	605	ArgblybTyrAangbAlaLeugbIleamabpThrlleatgmetlleasbAlatyrThr	624
Db	1042	AGCGGCTTCAATTGACGGCCTCTCTATCATACACCGTCCGGCGGCTGGATGCTTGCTGCT	1101
QY	625	HibLeugIuthrphetTyrAangIuGluIblybAspIbysbPheAlaVallleGluAspAsp	644
Db	1102	GCGCTGACGAGATTCTATCACAGGAGACGTCATAAACCCAGATCTCTG-----	1152
QY	645	SerbAspGluGlyGlybAspAspGluTyrCybAspGlybAspGluAspGluAspLeuIbys	664
Db	1153	-----TGT-----	1155
QY	665	LysbProleuIblybLeuAspGluThrAspAspPheLeuMetThrlLeupbPheGluAsnAsn	684
Db	1156	-----GCCAGCGCGGCTGCTGGCGCTCTGTCGATGACCGCAAG	1199
QY	685	LysMetLeuIblybArgLeuAlaGluAsnProGluTyrGluAsnGluIblybLeuThrIblybLeu	704
Db	1195	AATGAGCTGGCGCCACTTGGCAATCATGGCCCA---GAGATTCAAAACCTGAGATGCTG	1251
QY	705	ArgbAsnThrlleMetGluGlnTyrThrArgThrlGluIuSerAlaargGlyllePhe	724
Db	1252	GAAAAAGATCTGCAAAAGCCAGTTCCAGT---AGCTTAACACCCCTCGGGGTATCATCTTC	1308
QY	725	ThrlbSthbTrrArgbInserAlaTyrAlaLeuSerGlnIhrlleThrgIuAsnGluIblybPhe	744
Db	1309	ACCGGACCCCGCCAAAGGCACTCCCTCTGCTGCTGCACGACGACGACGAGGCTG	1368
QY	745	AlaGluValbGlybAlaIbAsnHibLeuIleGlyAlaGlyHibSerSergIuPheIbys	764
Db	1369	CAGACTGGACATCCCGGCGCCACTACTGATTTGGGCTGGGAGACAGACGACAGACACC	1428
QY	765	ProMetThrgIuAsnGluGlnIblybGluValleSerybPheargThrgIyIbAsn	784
Db	1429	CACATGACCCGACGAGGACACGACAAAGATGATCCAGAAATTCGAAATGGAACCTTGAC	1488
QY	785	LeuIuIleAlaThrlThrValAlaGluGlnIblybLeuAspIleuIblybGluCybAsnIleVal	804
Db	1489	CTTCTGGTGGCACGAGTGTGGCGAGAGGAGGCTGGACATCCACATTCGAAATGTGTG	1548
QY	805	IleatgTyrGlyLeuValAlThrAsnGluIleAlaMetValGlnAlaArgGlybArgAlaarg	824
Db	1549	GTGGCTTATGGGCTCTTGACCAATGAATCTCCATGTGTCCAGGCGCAGGGCGCTGCCCG	1608
QY	825	AlaAspGluSertThrTyrValleuValAlaHibSergIySergIyVallleGluHibGlu	844
Db	1609	GCCGATCAGATGTATATAGCGCTTTGTAGCAACTGAAGGTATAGCCGAGACCGGAG	1668
QY	845	ThrValAsnAspPheAlaargGluIblybMetMetTyrIblybAlaIleHibCybValGlnAsnMet	864
Db	1669	CTGATCAACGAGGCGCTGGAGACCCCTATATGAGCAGCAGCAGCTGCTGTGCACAAAATG	1728
QY	865	LysbProGluGluTyrAlaIbAsnIblybIleLeuGluIuMetGlnIuMetGlnIuMetGluIbys	884
Db	1729	GACCAAGCCGAGTATCCAGGCCCAAGATCCGGATTTGCAGCAGGACGACCTTACCAAGCG	1788
QY	885	LysMetIblybThrlbArgAsnIleAlaIblybHibTyrIblybAsnAsnProSertLeuIleThr	904
Db	1789	GCGGCGCCAGCGCCAGCGGAGAACACAGCGGACAGATTCACAGTGGACAGCTGCAG	1848
QY	905	PheIuCybIblybAsnCybSertValleuAlaCybSertGlybAspIleHibAlalleGlu	924
Db	1849	CTACTCTGCATCACTGATGTGGCTGTGGCGCATGGCAGCGACCTGCGGAAGTGGAG	1908
QY	925	LysMetHibHibValAsnMetThrProGluPheGluIuMetTyr---IleValArgIu	943
Db	1909	GGCACCCACATGTCATATGGAACCCCACTTCTCGAACTATATATGTCTCCAGGGAT	1968
QY	944	AsnIblybAlaLeuGlnIblybCybAlaAspTyrGlnIleAsnGluIuIleCybIbys	963

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DB 1969 CCTGTGTCATACAAAGTCTTCAAGACCTGCGGGGTCTCATCAGCTCAGG 2028
QY 964 ---CAGGlyGlnAlaTrpGlyThrMetMetValHisIleGlyLeuAspLeuProCysIleu 982
DB 2029 AACTGTGGGAGAGTCTGGGGTCTGCAGATGATCTTACAACTGAGAGCTGCGAGTCTC 2088
QY 983 LysIleArgAspPheValValPheLysAsnAsnSerThrLysGlnTrpLysLys 1002
DB 2089 AAAGTCCGACG-----ATGCTGCTGAGAGACCCCTCAGGGGCGGATCCAGGCCAATAAG 2142
QY 1003 TTPValGlnLeuProIleThrPheProAsnLeuAspTrpSerGluCys 1019
DB 2143 TGTGTCGCGGCTCTTCTCCGCTGCTGACTTGTCTGCTGAGCATTTGT 2193

RESULT 3
US-09-907-907A-32
; Sequence 32, Application US/09907907A
; Patent No. 6951923
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Leszczyniecka, Magdalena
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESENCE
; FILE REFERENCE: A34584-A-PCT-USA (070050.1664)
; CURRENT APPLICATION NUMBER: US/09/907,907A
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 09/243,277
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 342, 355, 365, 368, 375, 381, 385, 414, 445
; OTHER INFORMATION: a or c or g or t
US-09-907-907A-32

Alignment Scores:
Pred. No.: 1,43e-45 Length: 458
Score: 498.00 Matches: 90
Percent Similarity: 98.9% Conservative: 0
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 9.4% Indels: 0
Gaps: 0
DB: 3

US-09-515-363c-2 (1-1025) x US-09-907-907A-32 (1-458)
QY 935 PheLysGlnLeuTrpTlleValAlaArgGlnAenLysAlaLeuGlnLysCysAlaAspTrp 954
DB 3 TTCACAGAACTTACATTTGTAAAGAAACAAACAACTGCAAGAGTGTGCGCATAT 62
QY 955 GlnIleAsnGlyGlnIleIleCysLysCysGlyGlnAlaTrpGlyThrMetMetValHis 974
DB 63 CAATTAATATGTTAAATTCATCTTCAATATGCGCAGGCTTGGGAAACATGATGTCAC 122
QY 975 LysGlyLeuAspLeuProCysLeuLysIleArgAsnPheValValPheLysAsnAsn 994
DB 123 AAAGGCTTGAATTTGCTGCTCAAAATAGGAATTTGTAGTGGTTTCAAAATTAAT 182
QY 995 SerThrLysLysGlnTrpLysLysLysTrpValGlnLeuProIleThrPheProAsnLeuAsp 1014
DB 183 TCACAAAGAAACAAATACAAAGAGTGGTGAATTAATCTATCATTTCCCAATCTTGAC 242
QY 1015 TyrSerGluCysLeuPheSerAspGlnAsp 1025
DB 243 TATTCAAGATGCTGTTATTAGATGAGGAT 275

RESULT 4
US-08-143-576-7
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; Sequence 7, Application US/08143576
; Patent No. 5643761
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Jiang, Hongping
; TITLE OF INVENTION: METHOD FOR GENERATING A SUBTRACTED
; TITLE OF INVENTION: CDNA LIBRARY AND USES OF THE GENERATED LIBRARY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/143,576
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43563/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-143-576-7

Alignment Scores:
Pred. No.: 5.3e-43 Length: 301
Score: 472.00 Matches: 97
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 8.9% Indels: 1
Gaps: 0
DB: 2

US-09-515-363c-2 (1-1025) x US-08-143-576-7 (1-301)
QY 476 LysProValIleProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGly 495
DB 3 AAACCAAGTATTCCTTCTTCAGATACAGGCTTCACTGCTGTGGAGGG 62
QY 496 AlaThrLysGlnAlaLysAlaGlnIleLysIleLeuLysLeuCysAlaAsnLeuAspAla 515
DB 63 GCCACAGAGCAACCCAAAGCTGAAGACATTTTAAACTATATGCTTATGATGCA 122
QY 516 PheThrIleLysThrValLysGlnAenLeuAspGlnLeuLysAsnGlnIleGlnIlePro 535
DB 123 TTACTATTAAACCTTTAAAGAAACCTTGATCAATGAAACCAATACAGAGCA- 181
QY 536 CysLysLysPheAlaIleAlaAspAlaThrArgGlnAspProPheLysGlyLysLeu 555
DB 182 TGCAGAGAGTTGCTCATTCAGATGCAACAGAGAGATCCATTTAAAGAAACTTCTA 241
QY 556 GlnIleMetThrArgIleGlnTrpLysGlnIleMetSerProMetSerAspPheGly 574
DB 242 GAATATATGACAAAGATTCAAACTTATGTCAATATGATCAATGTCAGATTGGA 298
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RESULT 5
US-09-221-268D-12
; Sequence 12, Application US/09221268D
; Patent No. 6720408
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Jiang, Hongping
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH SPECIFICALLY HYBRIDIZE WITH
; FILE REFERENCE: A34534-8-A (070050.1537)
; CURRENT APPLICATION NUMBER: US/09/221,268D
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 08/316,537
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: 08/143,576
; PRIOR FILING DATE: 1993-10-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 301
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-221-268D-12

Alignment Scores:
Pred. No.: 5,3e-43 Length: 301
Score: 472.00 Matches: 97
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 8.9% Indels: 1
DB: 3 Gaps: 0

US-09-515-363C-2 (1-1025) x US-09-221-268D-12 (1-301)

QY 476 LysProValIleProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGlyGly 495
DB 3 AAACCAAGTATCTCCCTCTCCTCAGATCTGGGACTAACAACCTTCACTGCTGGTGGAGG 62

QY 496 AlaThrIleGlnAlaIleValIleGlnIleIleLeuIleLeuGlyValAlaLeuAlaPro 515
DB 63 GCCACAGACGACCAACCAAGTGAAGAACACATTTTAAACTATGTGCTATCTTGATGCA 122

QY 516 PheThrIleLeuThrValIleGlnIleLeuIleLeuAspGlnIleLeuIleLeuIlePro 535
DB 123 TTTACTATTAACTGTTTAAAGAAACCTTGATCACTGAAAAACCAATACAGAGCA- 181

QY 536 CysIleIlePheAlaIleAlaAspAlaThrArgGluAspProPheIleGlyIleLeu 555
DB 182 TGCAGAGAGTTTCCATTGCAATGCAACAGAGAACATTCATTAAAGAAACCTTCTA 241

QY 556 GluIleMetThrArgIleGlnIleIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 574
DB 242 GAATATATGACAAGATTCAACTTATGTCAATATGATCAATGTCAGATTTTGA 298

RESULT 6
US-09-590-968B-1
; Sequence 1, Application US/09590968B
; Patent No. 6737561
; GENERAL INFORMATION:
; APPLICANT: Golden, Teresa Ann
; APPLICANT: Ray, Animesh
; TITLE OF INVENTION: GENE ENCODING SHORT INTEGUMENTS AND USES THEREOF
; FILE REFERENCE: 176/60581
; CURRENT APPLICATION NUMBER: US/09/590,968B
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/138,316
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6184
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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US-09-590-968B-1

Alignment Scores:
Pred. No.: 2,06e-33 Length: 6184
Score: 406.00 Matches: 231
Percent Similarity: 39.8% Conservative: 158
Best Local Similarity: 23.6% Mismatches: 316
Query Match: 7.6% Indels: 275
DB: 3 Gaps: 47

US-09-515-363C-2 (1-1025) x US-09-590-968B-1 (1-6184)

QY 20 AlaArgValIleMetThrIleGlnValGluProValIleuAspThrIleuThrPheLeuPro 39
DB 127 TCTAGGGTTTGGTCTCTCTCTTCTTCCGAGCCCC-----TTTAAACCT 168

QY 40 Ala-----GluValIleGlnIleGlnArgThrValAlaThrSerGlyAsnMetGln 57
DB 169 GCMAACACAACTTCAAAATTGGCGGTTCGACGGCTTA-TCTAACCTTAATCTGTCA 227

QY 58 AlaValGluLeuLeuLeuSerThrLeuGlnIleGlnValIleThrPheIleGlyThrArg 77
DB 228 CAAAACACTCTTCTTCTTCTCACCCCTTTTGGGTTATTCAT-----TCTCGT 278

QY 78 GluPheValGluAlaLeuArgThrGlySerProLeuAlaAlaArgThrMetAsnPro 97
DB 279 GCTTTT-----GGTTCTGTTTCTTCTCTGGG 305

QY 98 GluLeuThrAspLeuProSerProSerPheGluAsnAla-----HisAspGlu 113
DB 306 GATTGGTTTCTGTG--AGTGAAGTTTCTCTCTTCTTATGTTCTTGATTTGATTTAT 362

QY 114 TyrLeuGlnIleu-----LeuAsnLeuLeuGlnPro-----ThrLeuVal 126
DB 363 TATATGAATTTATGTAATGAGATGACCTTAAGAACCAATAAACCTTCTTAT 422

QY 127 AspIleLeuLeuValIleArgAspValIleuAspIleCys--MetGluGluLeuLeuThr 145
DB 423 CGCTAGATGCTTGC-GAGGACATC-----TCTTGATCTTATTCATGATCTCGTGT 475

QY 146 IleGluAspArgAsnArgIleAlaAlaGluAsnAsnGlyAsnGluSerGlyValArg 165
DB 476 GAATTGATCTTCTCTCTGCTGCTGCTCAATGATTCACCT--GATAAAAAGGCGTC-- 529

QY 166 GluLeuLeuIleValIleValGlnIleGlnIleLeuIleLeuIleLeuIleLeu 185
DB 530 -----ATCAATGATTTTTCGTCGATTCATTCATTTA 565

QY 186 ArgGlnThrGlyAsnAsnGluLeuValGlnIleuThrGlySerAspCysSerGluSer 205
DB 566 GATAGTATCAAGAACGCT-----GGAGCGCTTCAACAACAAATGGCGTTCTGATACC 616

QY 206 AsnAlaGluIleGluLeuLeuSerGlnValAspGlyProGlnValGluGlnIleuLeu 225
DB 617 AATTCTCAATCAACAGGTTACTGTACT-----CTCAGGTT-----ATTGCT 661

QY 226 SerThrThrValGlnProAsn--LeuGluIleGluValIleIleGluIleuAsnSer 244
DB 662 AAGAGACAGCTGAAGAGATGGTTGCAAAAGATGGCGGTAAAGAGACGAATTCCTG 721

QY 245 SerGluSerSerPheAlaAsp-----SerSerValIleSerGluSer 258
DB 722 AAGAGAGAGAGACACAGATTAAGAGAGACGTAAGGTTTGTATATACGATGAAG 781

QY 259 AspThrSerIleuAlaGluIleSerValSerCysLeuAspGlu----- 272
DB 782 AGTACCTTTCAGGTAGAGGCGATGTTAATATTTTACGAGAGGAGATAGTTATGAAT 841

QY 273 -----SerLeuGlyHisAsn----- 277
DB 842 AGGAAACGTAATCGTAATTGGAGCGAGCGGTAAACATTAAGAGAAAGGGAATGTAC 901

QY 278 -----SerAsnMet 280

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Db 902 AATTACAGAGAGATGTAGATAGAGAAATTGAGGATTATTCGAGAGCGATMAAGTT ...
Qy 281 GlycerAsp-----SerglyThermGlySerAsp----- 292
Db 962 GGTTCCAAATGAGTGGTTTATATAGTCAGGACTTGGGAAGCTGATCATGAAGATGTT 1021
Qy 293 -----GluGluAsnValAlaAla 298
Db 1022 AAGAAAGTAGTGTTGAGAAACCGGAATGCATGCATCAAGCAGAGGAAAC----- 1072
Qy 299 ArgAlaSerProGluPro-----GluLeuGlnLeuArgProTyrgln 312
Db 1073 AAGAGTACCTGTAACAGTAAGAAAGAGTTGTGTAAGAGCAACAGCCATCCAG 1132
Qy 313 MetGluValAlaGlnProAlaLeuGluGlyLeuAsnIleIleIleCysLeuProTyrGly 332
Db 1133 TTGGATGTTCTTGACAAAGCT--AAAGCAAAAACACGATTCCTTCTTGAGACCGGT 1189
Qy 333 SerGlyLeuThrArgValAlaValTyr-----IleAlaLysAspHisLeuAsp 348
Db 1190 GCTGGAAAGACCTTATCGGATCTTCTTATTAAGAGTTCAATAGATCTGATGAGC 1249
Qy 349 LysLysLysLeuAspSerGluProGlyLysValIleValLeuValAsnLysValLeu 368
Db 1250 CAGAACAGAAAATGCTCTCG-----GTGTTCTTGCTCCCAAGTCCCTTGG 1297
Qy 369 ValGluGlnLeuPheArgLysGlu-----PheGlnProPheLysLys 383
Db 1298 GTTATTCAGCA-AGCAAGATGATCCGTATCAAACTGTTTCAAGTTGGAATATTC 1356
Qy 384 TTPYArgValIleGlyLeuSerGlyAspThrGlnLeu-LysIleSerPheProGluVal 403
Db 1357 TGGTGAGATGGGACAGACTTTGGGATCTCGAGGTGCAAGTGGCAAGAGATT----- 1408
Qy 403 ValLysSerCysAspIleIleIleSerThrAlaGlnIleLeuGlnAsnSerLeuLeu 423
Db 1409 ---GAGTCAAGCAGGTTCTAGTTATGACAGCACAAAATCTGTGAAATATCTG----- 1459
Qy 423 IleuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeuIleIleLeu 443
Db 1460 -----AGACACGATTCATTAAGATGAAACAAATTGATCTTATTCCTCA 1506
Qy 443 PGIuCyHisIleThrAsnLysGluAlaValTyrAsnAsnIleMetArgHisTyrLeu 463
Db 1507 CCACTGTACCAACGCTGTCAAGAAACATCATCTTTAGTATGTCAGAGTTTACCA 1566
Qy 463 CgluLysLeuLysAsnAsnArgLeuLysLysGluAsnLysProValIleProLeuProG 483
Db 1567 TACAACTCCTAAAGATMAAGA-----CCTGC 1593
Qy 483 nileuGlyLeuThrAlaSerPro---GlyValGlyAlaThrLysGlnAlaLysVal 502
Db 1594 CATCTTTGGATGATGCTGCTGCTTTAAATTAAAGGGTTCCTCAAGCCAAAGTAGTTC 1653
Qy 502 agluGluHisIleLeuLysLeuCyAlaAsnLeuAspAlaPheThrIleLysThrVally 522
Db 1654 TGGGATTAAGATATGTAACCTCGAGACCAAGTTGATTC--ACGGTTTGTACTATAA 1710
Qy 522 ggluAsnLeuAspGlnLeuLysAsnGlnIleGlnGluProCysLysLysPheAlaIleAl 542
Db 1711 AGATCA---AAAGAAATTAGAGAAACATGTGCTATGCTTCAGAGATAGTCTCGAGTA 1767
Qy 542 aaPp---AlaThrArgGluAspProPheLysGluLysLeuGlnIleMetThrArgAl 561
Db 1768 TGCAAAAGCTGCTACTATGTGCTCTTCTCATGAACAATAAGCAAAATGTTGCACTGT 1827
Qy 561 eglInThrTyrCysGlnMetSerPheMetSerAspPheGlyThrGlnProTyrGluGlnTr 581
Db 1828 TGAAGAAGCGGCAAGCAAGTTCAAGAAA-----AGCAAGTG 1866
Qy 581 palalIleGlnMetCgluLysLysAlaLysLysGlyAsnArgLysGluArgValCyAla 601

Db 1867 GCAATTTATGGGGCTAGGAGATGCTGAGCAAAAGATGAATTGACAGATTATGCGCT 1926
Qy 601 agluHisLeuArgLysTyrAsnGluAlaLeuGlnIleAsnAspThrIleArgMetIleAs 621
Db 1927 CTCTGAAAGACGAGAGAGGATGTGCTCCCAATTTGATTCATTAACATGAGCTATCA 1986
Qy 621 P-----AlaTyrThrHisLeuGluThrPhe----- 629
Db 1987 TTATACTTGTCTGAATTGGTCAATGTGTGCTTCAAGGTGGGCAATCATCTTGTTC 2046
Qy 630 -----TyrAsnGluLysAspLysLysPhe----- 638
Db 2047 TGCTTGCAAAGTAGAGAGAGGTGAATTTCCAAAGTCACGTGAATTCAGAAATCAT 2106
Qy 639 -----AlaValIleGlu-- 642
Db 2107 CCTCAGTAGAGTGTGTCACTGTTCGATGTGAGCTTTCGAAGGCGCTGCTGTAATA 2166
Qy 643 -----AspAspSerAspGluG 648
Db 2167 AGTCGGCGCGGAAGTTGGCAACAGAAAATGTATGCAATGACATGAGAAATGAGAGG 2226
Qy 648 Y-----GlyAspAspGluTyrCysAspGlyAspGluAspGluAspLysLysP 666
Db 2227 AAGACTCCCTGATGATCTCTGTGTCTCGAGGAGGAGCACTTGATGAAGTATAGCC 2286
Qy 666 oleuLysLeuAspGluThrAspArgPheLeuMetThrLeuPheGluAsnLysPhe 686
Db 2287 CGCAGTGGCTGAT-----GGGAAAGT 2307
Qy 686 CleuLysArgLeuAlaGluAsnProGluTyrGluAsnGluLysLeuThrLysLeuArg 706
Db 2308 TACTCCAAAAGA-----CAATCATGATCAAACTA----- 2338
Qy 706 nThrIleMetGluGlnTyrThrArgThrGluGlnSerAlaArgGlyIleIlePheThrly 726
Db 2339 -----CTCCCAAAATACAGACACAGCTGAT--TTCCAGCATTTGTTTCCTGA 2388
Qy 726 sThrArgInserAlaTyrAlaLeuSerGlnTrrIleThrGluAsnGluLysPheAlaG 746
Db 2389 AGGGGTGGTGGCTGTGGTTCTCT-----AAGTTTTCCGGA 2430
Qy 746 uValGly-----ValLysAlaHisIleLeuIleGlyAlaGlyHisSerG 762
Db 2431 GCTGCTTGGCTTATGTTATACGGTGTCCAGCAGATGTCACAAATMAACGCCAGA 2490
Qy 762 uPheLysProMetThrGlnAsnGluLysGluValIleSerLysPheArgThrGlyLys 782
Db 2491 GATGAAA-----TCATCTCAATGCAGATACAAATTTCCAAATTCGAGATGGCA 2541
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RESULT 7
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Buit et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; Patent No. 6503729
; TITLE OF INVENTION: jannaeschli
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
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US-08-916-421B-1

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Best Local Similarity: 23.0% Mismatches: 241
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QY 326 IleIleCysLeuProThrgIseGrgIyVtHrArGValAlaValIryIleAlaLysAsp 345
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QY 346 HisLeuAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 365
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QY 406 SerCysAspIleIleIleSerThraIagInIleLeuGlnAsnSerLeuLeuAsnLeuGln 425
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QY 614 AsnAspThryIleArgMetIleAspAla-----TythrHisLeuGln 627
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Qy 554 LeuLeuGluIleMetThrArgIleGlnThrCysGlnMetSerProMetSerAspPhe 573
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Qy 574 GlyThrGlnProCysGluGlnThrAlaIleGlnMetGluSlySlySlySlySlySly 593
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659537 ----- 1659537
Qy 594 AsnArgIlyeGluArgValCysAlaGluIleLeuArgIlyeThrAsnGluAlaLeuGlnIle 613
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659538 -----GATGAGAGAGTGAAGTATGAACCTTATTAAGTTGTTCAAGAGCTTTAAACTT 1659591
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 614 AsnAspThrIleArgMetIleAspAla-----TyrThrHisLeuGlu 627
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659592 ATGCATGCCCAAGACCTTAGAGAGTCAAGAAAGAGTATTTTAAACTATATTAAT 1659651
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 628 ThrPheThrAsnGluGluSlySlySlySlySlySlySlySlySlySlySlySlySly 647
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659652 AATTATTCATGCAAGAACCAATATCAGTAAATCTATGTTATATGATGA-- 1659702
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 648 GlyGlyAspAspGluCysAspGlyAspGluAspGluAspAspLeuSlySlySlySlySly 667
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659702 ----- 1659702
Qy 668 LysLeuAspGluThrAspArgPheLeuMetThrLeuPheGluAsnSlySlySlySlySly 687
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659703 AAAGTTAGAGAGCGAGTATATTATTAATGAATCAGATGTAAACATCCAAATTA-- 1659759
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 688 LysArgLeuAlaGluAsnProGluCysGluSlySlySlySlySlySlySlySlySlySly 707
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659760 -----GTTAAAGTGTGATGATGTTAAATAAT 1659786
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 708 IleMetGluGlnIlyThrArgThrGluGlnIleSerGluAlaArgIlyIleIlePheThrIlySly 727
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659787 ATTTTGCAAAA-----AATAGAGATGAGAAATTTATCTTGTCTCAATAT 1659834
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 728 ArgGlnSerAlaThrAlaLeuSerGlnIlyThrGluSlySlySlySlySlySlySlySly 747
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659835 AGGACACCTGTAGAGAAAGATTGTAATCTTAACTCAAAAT----- 1659876
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 748 GlyValIlySlyAlaHisIleSlyIleGlyAlaGlyHisSerGluPheIlySlySlySlySlySly 767
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659877 GGAATTAAGCAATTAAGATTATTAAGACAGCA--AATTAAGAGAGAAAGGAGATGAGT 1659933
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 768 GlnAsnGluGlnIlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 787
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659934 CAGAAAGAGCAAAATAGAGCTTAAGAGATTAAAAA--GAGGGAAGTGTGTTAGTT 1659990
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 788 AlaThrThrValAlaGluGluGluIlyLeuAspIlyeSlyGluCysAsnIleValIleArgIly 807
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1659991 TCAACAGAGCTTCTGAGGAGGAGATGATTCATCGTAAATTAATCAATATTTTAT 1660050
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 808 GlyLeuValThrAsnGluIleAlaMetValGlnAlaArgIlyArgAlaAspGlu 827
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660051 GAACCACTGCCATCAGAAATTTAGTTTATTCAGAGAGAGAGTGAAGGAGAGAGAGAA 1660110
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 828 -----SerThrTyrValIleVal-----AlaHisSerGlySer 838
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660111 GAGAGGAGAGCTTATGTTTAAATAGCTTAAGAGAAAGAGCTGATGAAGCTTATTCAGAGAGT 1660170
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 839 GlyValIleGluIlySlyGluThrValAsnAspPheArgGluSlySlyMetCysIlySlyAlaIle 858
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
Db 1660171 GCTTTATACAAAGAGAGATGAAGAGATTATTAATAATATGTTATTTCTTAAT 1660230
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 859 HisCysValGlnAsnMetLysProGluGluIlyThrAlaHisIleIleLeuGluLeuGlnMet 878
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660231 AAGAGCTTACAGAG--AAATTTAGAGAAATCTTAAGAGAAATTAAGAGAGAGACA 1660287
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 879 GlnSerIleMetGluIlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 897
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660288 GAAGAAATTAAGAGAAAGAAATTAAGATCAAAAATCGCATTAAGAGAGAAAGAGAGAG 1660347
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 898 -----AsnAsnProSerIleIleThrPheLeuCysIlySlySlySlySlySlySlySly 912
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660348 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660407
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 913 -----LeuAlaCysSerGlyGluAsp----- 919
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660408 AAGAGAGAGCTTAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660467
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 920 ----IleHisValIleGluIlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 933
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660468 CCAATTAAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1660527
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 934 -----GluPheIlyeGluLeu-----TyrIleValArgIlySlySlySlySlySlySly 946
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660528 GCAAAATATTGAGCTTAATAAAACATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660587
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 947 LeuGlnIlySlyCysAlaAspIlyThrGlnIleAsnGluIle 960
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1660588 GTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660629
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 9
US-09-853-768-3
; Sequence 3, Application US/09853768
; Patent No. 6444466
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION
; FILE REFERENCE: RTS-0217
; CURRENT APPLICATION NUMBER: US/09/853,768
; CURRENT FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 3
; LENGTH: 7037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)...(5957)
US-09-853-768-3

Alignment Scores:
Pred. No.: 1,71e-25 Length: 7037
Score: 335.50 Matches: 186
Percent Similarity: 36.5% Conservative: 113
Best Local Similarity: 22.7% Mismatches: 233
Query Match: 6.3% Indels: 288
DB: 3 Gaps: 43

US-09-515-363c-2 (1-1025) x US-09-853-768-3 (1-7037)
Qy 309 ArgProTyrGlnMetGluValAlaGlnProAlaLeuGlnIlySlySlySlySlySlySlySly 328
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 315 AGAAATATACAGGTTAACTGCTTGAAGAGAGCTGAG--CATATCCATCGTCTG 371
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 329 LeuProThrGlySerGlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 345
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 372 TTAACACTGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 346 HisLeuAspIlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 364
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 432 TATCTGATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```


Db 2205 TCACCTCTTCGAGCCTTCATTTGTTGCACCAATGAGCTGTGTACGATTGCTGAAGA 2264
Qy 976 yleuapleuPro-----CyleuylsileargAsnPhenValVal 990
Db 2265 GTTGTGCTTCATTTGCTGTGTGAGAAACCTGCACAAATTTGGCAACTGATGACCAATT 2322

RESULT 10
US-09-408-020-65
Sequence 65, Application US/09408020
Patent No. 6632937
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCPOR.002A
CURRENT APPLICATION NUMBER: US/09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 65
LENGTH: 1512
TYPE: DNA
ORGANISM: Cenarchaeum symbiosum
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1512)
US-09-408-020-65

Alignment Scores:
Pred. No.: 1,52e-21 Length: 1512
Score: 289.50 Matches: 137
Percent Similarity: 39.4% Conservative: 88
Best Local Similarity: 24.0% Mismatches: 188
Query Match: 5.5% Indels: 158
Gaps: 23

US-09-515-363c-2 (1-1025) x US-09-408-020-65 (1-1512)

Qy 303 GluPro---GluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeuGlu 321
Db 34 GAGCCCGGCGCCCTCGAGAGCCCGCACTACCAAGTGGCCCTTGCAGAGCAAGCATACGG 93
Qy 322 GlyLysAsnIleIleIleCysLeuProThrGlySerGlyIleThrArgValAlaValTyr 341
Db 94 ---GAAAACTGATAGTGTGTGCTGCTACCGGCTCGCAAGACGCGCGTGCAG 150
Qy 342 IleAlaLysAsnIleLeuArgLysLysLysAlaSerGluProGlyLysValIleVal 361
Db 151 GTATGTCCCACTATTGTGACGAAGCGGGGGCTCTCTTCTTGGCCGACAAAGGTTG 210
Qy 362 LeuValAsnLysValIleuValGluGlnLeuPheArgLysGluPheGlnProPheLeu 381
Db 211 CTGTAAAC-----CAGCACCGCCAGTCTCTG 237
Qy 382 LysLysTrpTyrArgValIleGlyLeuSerGlyAspThrGlnLeu-----LysIleSer 399
Db 238 GGC-----AGGGCCCTTACCATATCCGATATTACCTGGTGCACAGGCGAGCACCC 288
Qy 400 PheProGluValValLysSerCys-----AspIleIleIleSerThrIleGlnIleLeu 417
Db 289 GTCCCGAGCGCGCAAAAGCTTGGGGCGGCGGACGTGATCTGCGCACCCCGAGATACAC 348
Qy 418 GluAsnSerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPhe 437
Db 349 AGAAGACACTAGCGCGC-----GGAATGGTCCCGCTCGAACAAGTTC 390
Qy 438 SerLeuIleIleIleArgGlyCysHisHisThrAsnLysGluAlaValTyrAsnAsnIle 457
Db 391 GGGCTGTGTGTTCGACGAGGCGCACAGGCGGCGTGGCGACTATGCTATTCGCAATA 450

Qy 458 MetArgHisIleTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysGluAsnLysPro 477
Db 451 GCG-----CGTGCAGTGGGGGAACTCT--- 474
Qy 478 ValIleProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGlyValAlaThr 497
Db 475 -----AGAAATGATCGGCATGATCTCGC----- 495
Qy 498 LysGlnAlaLysAlaGluGlnHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThr 517
Db 496 -----ACC 498
Qy 518 IleLysThrValLysGluAsnLeuAspGlnLeuLysAsnGlnIleGlnGluProCysLys 537
Db 499 CTTCACGAGGAGGAGGAGAAAGCCGACGATATAGGCGACTTCTTCGAAG----- 552
Qy 538 LysPheAlaIleAlaAspAlaThrArgGluAsnPro----- 549
Db 553 -----AGCATAGCACAAAGGACCGGAAGACGCCGATGAAGCCCTACGTGCAGAG 606
Qy 550 -----PheLysGluLysLeuLeuGluIleMetThrArgIleGlnThrTyr 564
Db 607 ACCGAAACTGATGATGATTAAGGTGAGCTGCCCCCGAGATGAAGATCCAAAGCTC 666
Qy 565 CysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGlnGlnThrAlaIleGln 584
Db 667 CTGAAAGATG-----GCCCTCGAC 684
Qy 585 MetGluLysLysAlaAlaLysLys-----GlyAsnArg-LysGluArg 598
Db 685 GAAAGATATCGGCGCTCAAGAGGTGCGGCTATGATCTCGCTCGCAACAGTGTCTCTCG 744
Qy 598 GlyAlaGluAlaGlnIleLeuArgLysThrArgGlnAlaGlnIleAsnAspThrIleArg 618
Db 745 GCTCTCTCGCCCTTGCAGTGTGCTTCAAGCGGGAACAGCGCGCGCAAAAGCTTTG 804
Qy 618 GMetIleAspAlaTyrThrHisIleuGlnLysThrPheTyrAsnGlnLysLys---AspLysLys 637
Db 805 TTCTACGCGATACGATACATATCGCGCTCAACATATTGAGGCGCACGCGGTCGACCGC 864
Qy 637 AspPhe-AlaValIleGluAspAspSerAspGlnGlyGlyAspArgGlyTyrCysAspGlyA 657
Db 865 TTTCTAAAGTTCGCGAGAGGACCGTCAAGAAAGAGG----- 902
Qy 657 AspLysAspGluAspAspLeuLysLys-ProLeuLysLeuAspGluLysThrAspArgPheLeu 676
Db 903 -----CGCGGTGTGTGACAGACTGTCTTCAAGAGACACAA----- 936
Qy 677 MetThrLeuPhePheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnProGluTyr 696
Db 937 -----AACTTTACAGGGGCGCATGCGCGCGCAAAAGCGCGCACAGCGCGCATG 987
Qy 697 GluAsnGluLysLeuThrLysLysLeuArgAsnThrIleMetGlnGlnTyrThrArgThrGlu 716
Db 988 GAGCATCAAAAGATACCAAAAGTTG-----GAA 1014
Qy 717 GluSerAlaArgGly-----IleIlePheThrLysThrArgGlnSerAla 731
Db 1015 GAGGCTGTGCGCGGCGCAAAAGCGCGGTGTCTTTACAAAGCTACAGAGACTGTCTGTC 1074
Qy 732 TyrAlaLeuSerGlnTrpIleThrGluAsnGluLysPheAlaGluValGlyValAla 751
Db 1075 GATTAAAT-----CACTCAAAAGCTGACAGCTGCGGAGATAACTCG 1116
Qy 752 HisHisLeuIleGly--AlaGlyHisSerSerGluPheLysProMetThrGlnAsnGlu 770
Db 1117 GGGATCTCATAGGAAGCGCGGAGAA-----AAGGCTCTCAAGCGAAGAAA 1164
Qy 771 GlnLysGluValIleSerLysPheArgThrGlnLysLysIleAsnLeuLeuIleAlaThrThr 790
Db 1165 CAGTGAAGACTGTCTCGCAAGATTCGCGCAACGGGGGAGTACAGTGTCTCGATTTACACA 1224
Qy 791 ValAlaGluGlnGluLeuAspIleLysGluCysAsnIleValIleArgTyrGlyLeuVal 810

Db 1225 GTGGGAGAGAGGCTCCACATATCGAGTAACCTGTGTATTCATATGACAAATGTC 1284
QY 811 ThrAsnGluIleIleIleValGlnAlaArgGlyArg---AlaArgAlaAspGluSerThr 829
Db 1285 CCAGAGTCGATTAAGTATGTGCGAGAGAGGCGAGACCGCGAGAAAGACGGCGGCGAAG 1344
QY 830 TyrValIeuValAlaHisSerGlySer 838
Db 1345 CTGCTGTACTGATGCGAAAGGGGACT 1371
RESULT 11
US-09-408-020-1
Sequence 1, Application US/09408020
Patent No. 6632937
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCOIP.002A
CURRENT APPLICATION NUMBER: US/09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 32998
TYPE: DNA
ORGANISM: Cenarchaeum symbiosum
FEATURE:
NAME/KEY: CDS
LOCATION: (7604)...(8908)
FEATURE:
NAME/KEY: CDS
LOCATION: (8961)...(9767)
FEATURE:
NAME/KEY: CDS
LOCATION: (10545)...(10922)
FEATURE:
NAME/KEY: CDS
LOCATION: (113944)...(14612)
FEATURE:
NAME/KEY: CDS
LOCATION: (18638)...(20149)
FEATURE:
NAME/KEY: CDS
LOCATION: (20554)...(20955)
FEATURE:
NAME/KEY: CDS
LOCATION: (20956)...(21834)
FEATURE:
NAME/KEY: CDS
LOCATION: (25151)...(26377)
FEATURE:
NAME/KEY: CDS
LOCATION: (27535)...(28002)
FEATURE:
NAME/KEY: CDS
LOCATION: (28065)...(29483)
US-09-408-020-1
Alignment Scores:
Pred. No.: 3,13e-19
Score: 289.50
Percent Similarity: 39.4%
Best Local Similarity: 24.0%
Query Match: 5.5%
DB: 3 Gaps: 23

QY 303 GluPro---GluLeuGlnLeuAspProTyrGlnMetGluValAlaGlnProAlaLeuGlu 321
Db 18671 GAGCCCGGCGCCGCTGAGAGGGCGCATACAGTGGCTTGGCAGAGCGCATACCG 18730
QY 322 GlyAsnIleIleIleCysLeuProThrGlySerGlyLeuThrArgValAlaValTyr 341
Db 18731 ---GAAATCTGCATCTGCTGCTTACCGGCTTCGGCAAGACGGCGCTGGCGAG 18787
QY 342 IleAlaLysAspHisLeuAspLysLysValAspSerGluProGlyLysValIleVal 361
Db 18788 GTGATCTCCACATATTGGACGAGGAGGGGGCTCTCTTCCTTGGCCGACAAAGGTG 18847
QY 362 LeuValAsnLysValLeuLeuValGluGlnLeuPheArgLysGluPheGlnProPheLeu 381
Db 18848 CTGGTAAC-----CAGACCGCCAGTTCTCG 18874
QY 382 LysLysTyrTyrArgValIleGlyLeuSerGlyAspThrGlnLeu-----LysIleSer 399
Db 18875 GGC-----AGGGCCCTTACCATATCCATATTAACCTGTGTACAGCGGAGACAC 18925
QY 400 PheProGluValValLysSerCys-----AspIleIleIleSerThrAlaGlnIleLeu 417
Db 18926 GTCCCGAGCGGCAAAAGACTTGGGGCGGACGGTGTCTGCGCCACCCCGAGATAAAC 18985
QY 418 GluAsnSerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPhe 437
Db 18986 AGAAACGACATACCGCGC-----GGAATGGTCCCGCTCGACACACTCT 19027
QY 438 SerLeuIleIleIleAspGluCysHisIleThrAsnLysGluAlaValTyrAsnAsnIle 457
Db 19028 GGCCTGTGTGTTCACAGAGGCCACAGGGCGGTGGCGGACATACCTATTCCGCAAT 19087
QY 458 MetArgHisTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysGluAsnLysPro 477
Db 19088 GCG-----CGTCAAGTGGGGGAACTCT--- 19111
QY 478 ValIleProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyValGlyAlaThr 497
Db 19112 -----AGAAATGATCGGCATGACTGCG----- 19132
QY 498 LysGlnAlaLysAlaGluGluHisIleLeuLysCysAlaAsnLeuAspAlaPheThr 517
Db 19133 -----ACC 19135
QY 518 IleLysThrValLysGlnAsnLeuAspGlnLeuLysAsnGlnIleGlnGluProCysLys 537
Db 19136 CTTCCAAAGCGAGGAGGAAAGCCGACGAGATATAGGCACTTCTCTCAAG----- 19189
QY 538 LysPheAlaIleAlaAspAlaThrArgGluAspPro----- 549
Db 19190 -----AGCATACACAAAGAACCGAAAGACCCGAGATGAAGCCCTACGTCAGGAG 19243
QY 550 -----PheLysGluLysLeuLeuGlnIleMetThrArgIleGlnThrTyr 564
Db 19244 ACCGAAATCGAATGATTAAGTGTGAGCTGCCCCCGAGATGAAGAGATCCAAAAGCTC 19303
QY 565 CysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGluGlnTrpAlaIleGln 584
Db 19304 CTGAAGATG-----GCCCTCGAC 19321
QY 585 MetGluLysValAlaLysLys-----GlyAsnArg-LysGluArg 598
Db 19322 GAAAGATATCGGCGCTCAAGAGTGGCGGTATGATCTGGCTCGAAGAGTGGCTTCG 19381
QY 598 GValCysAlaGlnIleLeuArgLysTyrAsnGluAlaLeuGlnIleAsnAspThrIleArg 618
Db 19382 GCTCTGCTCCGCTTCCGATGCTGCTTCAAGCGCAACAGGGGGCGGAAACCTTGG 19441
QY 618 GMetIleAspAlaTyrThrHisLeuGluThrPheTyrAsnGluGluLys---AspLysLys 637
Db 19442 TTTAATCGCATACATACATACGAGCTCAACATATTCAGAGGCCAGGGGTACACCGCG 19501
QY 637 sPhe-AlaValIleGluAspAspSerAspGluGlyLysAspAspGluTyrCysAspGly 657

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Db      19502 TTTCTAAAGTTCTGCAGAGAGACCGTCAAGAAAAAGCG----- 19539
QY      657 spGluAspGluAspAspLeuLys- ProLeuLysLeuAspGluThrAspArgPheLeu 676
Db      19540 -----CGCCGGTGTTCAGAGCTGTTCAGAGAGACAG----- 19573
QY      677 MetThrLeuPheGluAsnAsnLysMetLeuLysArgPheLysGluAsnProGluLys 696
Db      19574 -----AAGCTTACAGGGCCATGCGCGCGCAAGCGCGCACAGCGCGCGCATG 19624
QY      697 GluAsnGluLysLeuThrLysLeuArgAsnThrLysMetGluGlnThrArgThrGlu 716
Db      19625 GAGCATCCAAAGATACCAAAAGTTG-----GAA 19651
QY      717 GluSerAlaArgLys-----IleIlePheThrLysThrArgGlnSerAla 731
Db      19652 GAGGCTGTGCGCGCGCGCAAGGAGCGCGCTGTTCACAGCTACAGGAGCTCTGTC 19711
QY      732 TyrAlaLeuSerGlnThrLysGluAsnGluLysPheAlaGluValGlyValLysAla 751
Db      19712 GATTATA-----CACTCAAGCTGAGGCTGCGCGGATAACTGC 19753
QY      752 HisHisLeuLysIleGly--AlaGlyHisSerSerGluPheLysProMetThrGlnAsnGlu 770
Db      19754 GGGATCTCATAGAAAGGCGGAGAA-----AAGGCGCTCAAGCAGAAAAA 19801
QY      771 GlnLysGluValLysLysLysPheArgThrGlyLysLysLeuLeuLysLeuLysLeu 790
Db      19802 CAGGTGAGAGCTGTCCCAAGTTCGCGCAGCGGCGATACGACGTGCTCGATATACAGA 19861
QY      791 ValAlaGluGluLysLeuAspLysLysGluCysAsnLysValLysArgThrGlyLysVal 810
Db      19862 GTGGCGGAGAGGCGCTCGACATATCGAGAGCTAAACCTTGCGTATTCATGACAAATGC 19921
QY      811 ThrAsnGluLysLeuMetValGlnAlaArgLysArg--AlaArgAlaAspGluSerThr 829
Db      19922 CCAAGCTCATATGATATGTCAGAGAGGCGCAGAGCCGCGCAGAAAGACGCGGCGCAG 19981
QY      830 TyrValLeuValAlaHisSerGlySer 838
Db      19982 CTGCTGTACTGTGCGCAAGGCGGACT 20008

RESULT 12
US-09-408-020-33
; Sequence 33, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOPT.002A
; CURRENT APPLICATION NUMBER: US/09/408,020
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Cenarchaeum symbiosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1509)
US-09-408-020-33

Alignment Scores:
Pred. No.: 6,17e-21 Length: 1509
Score: 284.00 Matches: 133
Percent Similarity: 41.4% Conservative: 94
Best Local Similarity: 24.3% Mismatches: 207
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Query Match: 5.3% Indels: 114
DB: 3 Gaps: 23
US-09-515-363c-2 (1-1025) x US-09-408-020-33 (1-1509)
QY      303 GluPro--GluLeuGlnLeuArgProLysGlnMetGluValAlaGlnProAlaLeuGlu 321
Db      34 GAGCCGCGTGTGCTGAGAGAGCGCGACTACAGGTGGCGGCGGAAACAGCGCATACCG 93
QY      322 GlyLysAsnLysLysLysLeuProThrArgLysGlyLysThrArgValAlaValLys 341
Db      94 ---GAGAACTGATCTGTGTCTCCGACGGGCTTCGGCAAGCTCCGTGCTCCAG 150
QY      342 IleAlaLysAspHisLeuAspLysLysLysAlaSerGluProGlyLysValLysAla 361
Db      151 GTGATCGCCCATATTCACAGAGCGCGCGGCGCGCTTCTCCCTTACAAAGGTC 210
QY      362 LeuValAsnLysValLeuLeuValGluLeuPheArgLysGluPheGlnProPheLeu 381
Db      211 CTGGTAAAC-----CAGCAGCGCGCTTCTG 237
QY      382 LysLysTrpTyrArgValLysLysLeuSerGlyAspThrGlnLeu-----LysLysSer 359
Db      238 GGC-----AGGCGCTTACCATATCCATATTCAGTGTCAAGGAGAGACACC 288
QY      400 PheProGluValValLysSerCys-----AspIleLysSerThrAlaGlnLysLeu 417
Db      289 ATTCCCGCGCGCAAAAGCGGTGGGAGCAGCGGTATTCGGCCACGCCGAGATAGCA 348
QY      418 GluAsnSerLeuLeuAsnLeuGlnLysGluAspAlaGlyValGlnLeuSerAspPhe 437
Db      349 AGAAATGATATA-----GAGCGCGCGCTGTCCGCTCGCAAGTTTC 390
QY      438 SerLeuLysLysLysLeuArgLysCysHisThrAsnLysGluAlaValLysAsnLysLeu 457
Db      391 GGCCTGTGATATTCACAGAGCGCGCAGCGCGGTGCGACTATCCATATTCCTCAT 450
QY      458 MetArgHisTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysGluAsnLysPro 477
Db      451 GCGCGG-----GCG 459
QY      478 ValIleProLeuProGlnLysLeuGlnLeuThrAlaSerProGlyValGlyLysAlaThr 497
Db      460 GTTAGGGATTAACCTCCAGATGATGGGCATGATCGACGCTT-----CCACAG 507
QY      498 LysGlnAlaLysAlaGluGlnHisLysLeuLysCysAlaAsnLeuAspAlaPheThr 517
Db      508 GAGAGCGAAGAGCAGACGAG-----ATATGCGCACCTGCTTCACAGAGC 555
QY      518 IleLysThrValLysGluAsnLeuAspGlnLeuLysAsnGlnLysGlnProCysLys 537
Db      556 ATAGCCCAAGAGACAGAAAGACCCGAGCGTAAAGCCCTATGATACAGAGACTGCCACC 615
QY      538 LysPheAlaIleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeuGlnLys 557
Db      616 GAGTGGATTAAGGTGATCTTCCCGCGAGATGAAGAGATACAGAGGCTCTCAAGCTG 675
QY      558 MetThrArgLysGlnThrLysCysGlnMetSerProMetSer--AspPheGlyThrGln 576
Db      676 GCCCTGCAC--GAGAGTATTCCTCCCTCAAGAGGTGCGGATGATCTTGCTCGCAAC 732
QY      577 ProTyrGluGlnThrAlaLysGlnMetGluLysValAlaLysLysLysLysAsnArgLys 596
Db      733 AGGTGCTGTGCGCGCTGCTCGGCTG--CGCATGTGTGTCTTGCGCGCAACAGCGCG 789
QY      597 GluArgValCysAlaGluHisLeuArgLysTyrAsnGluAlaLeuGlnLysLeuAsnArgThr 616
Db      790 GCG-----GCCAAGCGCGCTTCACTGCGCATACGATACGATACGCGG 831
QY      617 IleArgMetIleAspAlaLys-----ThrHisLeuGluThrPheTyrAsnGluLys 634
Db      832 CTAAACATATTCAGAGCGCAGCGGCTCAGCGCTTCTTAAAGTTCTGCGAGAGACCTCC 891
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Oy      635  AspIySlySPhaeIaValIleGIuAspAserAerAerGIuGIyGIyAspAerGIuTyCyS  654
           |||||
Db      892  AAGAAAAAGGCGTCGCGCGTGGCGAG----- 918
Oy      655  AspGIyAerGIuAspGIuAspAerLeuLySProLeuLySLeuAerGIuThrAspArg  674
           |||||
Db      919  -----  CTTTGAACAGACGCG  936
Oy      675  PheLeuNetThrLeuPhePheGluAenAenLySHeCLeuLySArgLeuAlGIuAenPro  694
           |||
Db      937  -----AACCTTAACAGGGCCATCGCGCGCGCAAGGCGCGACAGCGCA  981
Oy      695  GIuTyrgIuAenGIuLySLeuThrLySLeuArgAenThrIleMetGIuGIuTyThrArg  714
           |||||
Db      982  GGCATGGACATCCCAAGATACCAAGCTCAGAGATGCCGTC----- 1023
Oy      715  ThrGIuGIuSerAlaArgLy-----IleIlePheThrLySThrArgGIuSerAlaTy  732
           |||||
Db      1024  -----CGCGGGGGCGCGGGGAAGCGCGTGTCTTTACAGACTATCGTGAATTCGTGCAC  1077
Oy      733  AlaLeuSerGIuThrIleThrGluAenGIuSPhaeIaGluValGIyValIyAlaHis  752
           ::::
Db      1078  CTCATA-----CACTCAAGACTCAAGCGCGCGGATTAAGTCCGGCC  1119
Oy      753  HisLeuIleGIy---AlaGIyHisSerSerGIuPheLySProMetThrGluAenGIuGI  771
           |||||
Db      1120  ATCTCGATGAGAAAGCGCGGAGAA-----AAGGCCCTTAACAGAGAAACAG  1167
Oy      772  LysGIuValIleSerLySPhaeArgThrGIyLySLeuAenLeuLeuIleAlaThrThrVal  791
           |||
Db      1168  GTGAGAGACTGTGGCAATTCCTGTGACGCGGGATACAGACGTGTGTATTCAGCAGGCTG  1227
Oy      792  AlaGIuGIuGIyLeuAerIleLySGIuCySAnIleValIleArgTyrgLyLeuValThr  811
           |||||
Db      1228  GCGCGAGAGGGGCTCGACATATCGGAGGTCCAACTGTGAATTTCTATGACATGTGCCA  1287
Oy      812  AenGIuIleAlaMetValGIuAlaArgLyArg---AlaArgAlaAerGIuSerThrTy  830
           ::::
Db      1288  AGCTGCATCAGTACGTGTCAAGAGGAGGGAGAACAGGCAAGAAAGACGCGCGAGGCTG  1347
Oy      831  ValLeuValAlaHisSerGIySer  838
           |||||
Db      1348  ATAGTATTGATGGCAAGGAGACG  1371

RESULT 13
US-09-408-020-2
; Sequence 2, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP. 002A
; CURRENT APPLICATION NUMBER: US/09/408,020
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42432
; TYPE: DNA
; ORGANISM: Cenarchaeum symbiosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(10421)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10625)...(11434)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11478)...(13046)

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Db 35009 GCGCG-----GCG 35017
Qy 478 ValIleProleuProGlnIleuGlyLeuThrAlaSerProGlyValGlyAlaThr 497
Db 35018 GTAGGGGATTAATCTCCAGAGTGTGGCATGATGCGAGCTT-----CCAGCG 35065
Qy 498 LysGlnAlaLysAlaGlnGlnIleuLysLeuLysCysAlaSerLeuAlaPheThr 517
Db 35066 GAGAGGGAGAGGCGCAGCGAG-----ATATAGGCGACCCCTGCTCTCAGAGCG 35113
Qy 518 IleLysThrValLysGlnLeuLeuAlaSerGlnIleuLysGlnIleuGlnProCysLys 537
Db 35114 ATAGCCCAAGAGCAGACAGAGCGAGCGGAGGTAAGCCCTATGATACAGAGACTGCGACC 35173
Qy 538 LysPheAlaIleAlaPheAlaThrArgGluAlaPheProPheLysGlnLysLeuGlnIle 557
Db 35174 GAGTGGATTAAGGTGATCTTCCCCCGAGATGAGAGATACAGAGGCTCTCAAGCTG 35233
Qy 558 MetThrArgIleGlnThrCysGlnMetSerProMetSer---AspPheGlyThrGln 576
Db 35234 GCCCTGAGC---GAGAGGTATTTCTCCCTCAAGAGGCGGGGTACATCTTGCGCTGAGC 35290
Qy 577 ProTyrGlnGlnIleThrAlaIleGlnMetGlnLysAlaAlaLysLysGlyAsnArgLys 596
Db 35291 AGGTGCTCTCGCGCTGCTCGCGCTG---CGCATGGTGTGCTTGCGCGGCAAGGCGC 35347
Qy 597 GluArgValCysAlaGlnIleuLysLysTyrAsnGlnAlaLeuGlnIleAsnArgThr 616
Db 35348 GCG-----GCCAAGCGCGCTGTTCATCTGCGATACGATACGATACGCGC 35389
Qy 617 IleArgMetIleAspAlaTyr-----ThrIleLeuGlnThrPheTyrAsnGlnLys 634
Db 35390 CTAAACATATTTCAGAGCGCGCGGGGTACCGCCCTTTCTAAAGTTCTCGCGAGAGACTCC 35449
Qy 635 AspLysLysPheAlaValIleGluAspSerAspGlnGlyGlyAspArgLysCys 654
Db 35450 AAGAAAAGGGCGCTCGCGCTGCGCGAG----- 35476
Qy 655 AspGlyAspGlnAspGlnAspLeuLysLysProLeuLysLeuAspGlnThrArg 674
Db 35477 -----CTGTTCCGAACGAGCGG 35494
Qy 675 PheLeuMetThrLeuPhePheGlnAsnAlaSerMetLeuLysArgLeuAlaGlnPro 694
Db 35495 -----AACTTACAGCGCGCATCGCGCGCAAGCGCGCGCGCGCGCA 35539
Qy 695 GluTyrGlnAsnGlnLysLeuThrLysLeuArgAsnThrIleMetGlnIleTyrThrArg 714
Db 35540 GGCATGAGCATCCCAAGATACCAAGCTGAGATGCCGTC----- 35581
Qy 715 ThrGlnGlnSerLysArgGly-----IleIlePheThrLysThrArgGlnSerAlaTyr 732
Db 35582 -----CGCGGCGCGCGGAGAAAGCGCGCTGCTTACGAGCTATCGTATCTGTCGAC 35635
Qy 733 AlaLeuSerGlnIleThrGlnAsnGlnLysPheAlaGlnValGlyValAlaHis 752
Db 35636 CTCAT-----CACTCAAGACTCAGCGCGCGGAGAACTCGGCG 35677
Qy 753 HisLeuIleGly---AlaGlnHisSerSerGlnPheLysProMetThrGlnAsnGln 771
Db 35678 ATCTGATAGGAAGAGGGGAGAA-----AAGGCGCTAAAGCAGAGAAACAG 35725
Qy 772 LysGlnValIleSerLysPheArgThrGlyLysIleAsnLeuLeuIleAlaThrVal 791
Db 35726 GTGGAAGCTGTGCAAAAGTTCGTGACGCGGGGTACACGCTGTGATGTGAGAGGCTC 35785
Qy 792 AlaGlnGlnGlnLysAspIleLysGlnCysAsnIleValIleArgTyrGlyLysValThr 811
Db 35786 GCGGAAGAGGCTTCACATATGCGAGGTACACTGTGATATTTCTATGCAATGTGCCA 35845
Qy 812 AsnGlnIleAlaMetValGlnAlaArgLysArg---AlaArgAlaAspGlnSerThrTyr 830
Db 35846 ACCTCATATGATACGATACGAGAGAGGAGGAGAAACAGGCGCGCGAGGCTG 35905

Qy 831 ValLeuValAlaHisSerGlySer 838
Db 35906 ATAGTATTGATGCAAGAGGAGCG 35929
RESULT 14
US-10-104-047-1641
; Sequence 1641, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1641
; LENGTH: 2354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1641
Alignment Scores:
Pred. No.: 1,51e-20 Length: 2354
Score: 283.50 Matches: 166
Percent Similarity: 35.2% Conservative: 116
Best Local Similarity: 20.7% Mismatches: 245
Query Match: 5.3% Indels: 277
Gaps: 35
US-09-515-363c-2 (1-1025) x US-10-104-047-1641 (1-2354)
Qy 235 LysGlnValIleTyrGlyMetGlnAsnAsnSerSerGlnSerPheAlaAspSer----- 252
Db 6 AAGAAACCGATGGGATGGAACCGTACCGGTTGAGCTGCTGCTCTACGATATCTGA 65
Qy 253 -----SerValValSerGlnSerAspThrSerLeuAlaGlnLysSerValSerCys 269
Db 66 CAGAACCTTCGCTGCTT-----GTGCGCTTATGACCGCAGCGCAAGAACG 113
Qy 270 LeuAspGlnSerLeuGlnIleHisAsnSerAsnMetGlySerAspSerGlyThrMetGlySer 289
Db 114 CTTTTCAGACGtGGGCG-----TCAGTATCTCCGATCATCTGGACTCCGGGTTGC 167
Qy 290 AspSer----- 291
Db 168 AGCTCCGAAGTACGAGACCTCAGAGCCTGGAGCTCAAGCGCGCTTGGCCAGCAGCA 227
Qy 292 -----AspGlnGlnAsnValAlaAlaArgAlaSerProGlnProGln 305
Db 228 GCGGAGCTCAGCTGAGTGCAGATGATGTGCTTGTGCGCGGCGTACAGAGCTGAG 287
Qy 306 LeuGln----- 307
Db 288 CCGCAGCTTGTCTAGAAATGCGGGTTCTGCACTCCGCGGCGCGCTTGGATTTAC 347
Qy 308 -----LeuArgProTyrGlnMetGlnValAlaGlnProAlaLeuGlnGly 322
Db 348 CTTACCAATTCGCCAGATGGGAGGATCAGAGCTGCACATTTCCGGGCTGCTG---TTT 404
Qy 323 LysAsnIleIleLysLeuProThrGlySerGlyLysThrArgValAlaValTyrIle 342
Db 405 TGCATATACCTGTGTGTCTGCTTACCGGATCGGAAACCTTTATTTCCCGCGGCTG 464
Qy 343 AlaLysAspHisLeuAspLysLysLysValAserGlnProGlyLysValIleValLeu 362
Db 465 ATGTACAAATTTTAC-----CGCTGTTCTTCAGAAAGGTGGCTTTCAAG 512
Qy 363 Val---AsnLysValLeuLeuValGlnGlnLeuPheArgLysGlnPheGlnProPheLeu 381

Db 513 GCCCCACGAAACCTTGTCACACAGC-----ATC 545
 Qy 382 LysLeuTrpTyrArgValIleGly-----LeuSerGlyAsp 393
 Db 546 GAGGCTTGCTACAGGTGATGGTATCCGCAATCCACATGGCCGAATGACAGGCTC 605
 Qy 394 ThrGlnLeuLysIleSerPheProGluValLysSerCysAspIleIleIleSerThr 413
 Db 606 ACACAGACTTCC---ACCAGGAAGAAATATGTCGACATGAGAGAGTCTTTCTTAC 662
 Qy 414 AlaGlnIleLeuGlnLysSerLeuLeuLysLeuLysGlnLysAspIleGlnValGln 433
 Db 663 CCTCAGGTATGTTAATGACTT-----TCTAGAGAGCTTGTCC 704
 Qy 434 LeuSerAspPheSerLeuIleIleLeuGluCysHisIleThrAsnLysGluAlaVal 453
 Db 705 GCTGCTGAATAAAGCTTATGATTGATGAAGCTCATAAAGCTCCGAAACTATGCT 764
 Qy 454 TyrAsnAsnIleMetArgHisTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysLys 473
 Db 765 TATTCGACAGTTGTAGAGAA-----CTAGCAAAATATGCAATCAGCTT----- 809
 Qy 474 GluAsnLysProValIleProLeuProGlnIleLeuGlyLeuThrLysAspProGly--- 492
 Db 810 -----AGAACTTGCTCTTAACTAGTCCACACAGGATAGT 842
 Qy 493 -----ValGlyGlyAla----- 496
 Db 843 GATATAAGGCTGTGCACAACTTATTACTAATCTGTAATTTGGCAGATAGAGCTTCGT 902
 Qy 497 -----ThrLysGlnAlaLysAlaGlnGluHisIle 506
 Db 903 TCTGAAGATTCTCCAGATATTGTCATATATTCATGAAAGAAAGTGAAGACTTATT 962
 Qy 507 LeuLysLeuCysAlaAsn-----LeuAspAla 515
 Db 963 GTTCCGCTGGTGAAGAACTTGACGCAATCCAAAGACTATATCCAGATTTTGGAATC 1022
 Qy 516 PheThrIleLysThrValLysGluAsnLeu----- 525
 Db 1023 TTTGCTCGTCTTGTGATCTCAGAGAAATGTTTGTATGAGAAAGGATATCCCAATCTTAACA 1082
 Qy 526 -----AerGlnLeu--LysAsnGlnIleGlnLysProCys 536
 Db 1083 AAATATCAGATAATCTGCGCAAGAGATCAGTTTAGGAAAAACCC-ATCTCCGATATATGT 1141
 Qy 537 LysLysPheAlaIleAlaAspAlaThrArgGluAspProPheLysGlnLysLeuGln 556
 Db 1142 -----GGGAATACACAAAGGCAATATCG---AGGAGAGTGTGCTATTT 1182
 Qy 557 IleMetThr-----ArgIleGlnThrTyrCysGlnMetSerPheMetSerAspPheGly 574
 Db 1183 GATTAGTTTATATCATGTTATGATGATTAATTTGACGAAAGGAAATGACATCTTATATT 1242
 Qy 575 ThrGlnProTyrGlnGlnIleAlaIleGlnMetGlnLysLysAlaLysLysGlyAsn 594
 Db 1243 TCTTCTGTTGTGGAATATATG-----ATGGAACCT-AAAGGATG----- 1280
 Qy 595 ArgLysGluArgValCysAlaGlnHisLeuArgLysTyrAsnGlnLysLeuGlnIleAsn 614
 Db 1281 -----ACACGGTCAAAAAAATATGAACTTGCCCAAAATGAA 1313
 Qy 615 AspThrIleArgMetIleAspAlaTyrThrHisLeuGlnLysPheTyrAsnGlnLysLys 634
 Db 1314 GACTTCATGAAGCTC-----TATATCATCTAGAGTGTATGTTTGCACGTACACGT 1364
 Qy 635 AspLysLysPheAlaValIleGluAspAspSerAspGlnLysLysAspArgLysCys 654
 Db 1365 -----AGTACTTCAGCAAAATGTAATTTCTGCTATCCAA 1397
 Qy 655 AspGlyAspGlnAspGlnAspLysLysLysProLeuLysLeuAspGlnThrAspArg 674
 Db 1398 CAAGGAGAT----- 1406

Qy 675 PheLeuMetThrLeuPhePheGlnLysAsnLysMetLeuLysArgLeuAlaGlnAsnPro 694
 Db 1407 -----AAAAATAAAATTTGTT----- 1424
 Qy 695 GluTyrGluAsnGlnLysLeuThrLysLeuArgAsnThrIleMetGlnGlnTyr----- 712
 Db 1425 ---TATATGATCCAAAGTTAAAGAAATTTGAAAGAACTTTATGATGACATTCAAAGTCA 1481
 Qy 713 -----ThrArgThrGlnGlnSerLysArgGlyIleIlePheThr 725
 Db 1482 TGGAAATGCTGAAACACTACTGAAAGAAACGTGAATGACACCGAGTTATGATCTTCTCT 1541
 Qy 726 LysThrArgGlnSerAlaTyrAlaLeuSerGlnTyrIleThrGlnAsnGlnLysPheAla 745
 Db 1542 TCATTTGCAAGATAGTGTTCAGAAATTTGCAGAAATCTTTACACATCAGCCCAATTATT 1601
 Qy 746 GluValGlyValLysValHisIleLeuIleGlyAlaGlnHisSerSer-----GluPhe 763
 Db 1602 AGAGTA-----ATGACTTTTGTGCGCCATGCTCAGAGGAAAGCAGC 1643
 Qy 764 LysProMetThrGlnAsnGlnGlnLysGluValIleSerLysPheArgThrGlyLysIle 783
 Db 1644 AAGGCTTTTACCAGAAAGCACTGAGAGTATGTAACAGTTTCTGACGCTGATAC 1703
 Qy 784 AsnLeuLeuIleAlaThrThrValAlaGlnGlnGlyLeuAspIleLysGlnCysAsnIle 803
 Db 1704 AACACGCTGTTTCTACTGCTGTGGGTGAAGAGTTGTGATATAGAGAAAGTTGATCTT 1763
 Qy 804 ValIleArgTyrGlyLeuValThrAsnGlnIleAlaMetValGlnAlaArgGlyArg--- 822
 Db 1764 ATATATGTTTGTATTCCTCCAGAAAGCCCAATTCCTTGTACACAAAGATGGTAGACT 1823
 Qy 823 AlaArgAlaAspGlnSerThrTyrValLeuValAlaHisSerGlySerGlyValIleGln 842
 Db 1824 GGCCTGAAACGTCAAGGACGATGATTATTCCTTTCGAAAGA----- 1868
 Qy 843 HisGluThrValAsnAspPheArgGlnLysMetMetTyrLysAlaIleHisCysValGln 862
 Db 1869 -----CGAGAGCAACGATTTATATATCAG-----ACTCAG 1898
 Qy 863 AsnMetLysProGlnGlnLysThrAlaHisLysIleLeuGlnLeuGlnMetGlnMet 882
 Db 1899 TCCACAAAGAAAGTATAT----- 1919
 Qy 883 GluLysLeuMetLysThrLysArgAsnIleAlaLysHisTyrLysAsnAsnProSerLeu 902
 Db 1920 ---AAGCTATTTCAAGTAAACAGGACGTCCTTCATTTTACCAAGAAAGTCCACAGAAAG 1976
 Qy 903 Ile 903
 Db 1977 GTT 1979

RESULT 15
 US-08-143-576-6
 Sequence 6, Application US/08143576
 Patent No. 5643761
 GENERAL INFORMATION:
 APPLICANT: Fisher, Paul B.
 TITLE OF INVENTION: METHOD FOR GENERATING A SUBTRACTED
 TITLE OF INVENTION: CDNA LIBRARY AND USES OF THE GENERATED LIBRARY
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White, c/o Cooper & Dunham
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/143,576
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43563/JPW/ACC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ. ID NO.: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-143-576-6

Alignment Scores:
Pred. No.: 3,28e-16 Length: 193
Score: 227.50 Matches: 50
Percent Similarity: 75.4% Conservative: 2
Best Local Similarity: 72.5% Mismatches: 10
Query Match: 4.3% Indels: 8
DB: 2 Gaps: 1

US-09-515-363C-2 (1-1025) x US-08-143-576-6 (1-193)

QY 947 LeuGlnLysLysCysAlaAspTyrGlnIleAsnGlyGlnIleIleCysLysCysGlyGln 966
DB 1 CTGCACAAAGAGGTGCTCCGACTATAA-ATTAATGGTGAATCATCTGCAAAATGTGCCAG 59
QY 967 AlaTTPGlyThreMetValHisLysGlyLeuAspLeuProCysLeuLysIleArgAsn 986
DB 60 GCTTGGGGAACATGATGGTGCAAAAGCCTTAGATTGCTCTCAAAATATAGGAAT 119
QY 987 PheValValPheLysAsnAsnSerThrLysGlnIleTyrLysLysTyrValGlnLeu 1006
DB 120 TTGTAGTGTGTTCAAAA-----TATCAACAAGAACTACAGTG 158
QY 1007 ProIleThrPheProAsnLeuAspTyr 1015
DB 159 GTAGATCTATCATCATTCACTGACTAT 185

Search completed: March 12, 2006, 06:36:44
Job time : 5367 secs

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